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April 28, 1999

Box Patent Application

Assistant Commissioner for Patents
Washington, D.C. 20231

Re: U.S. Non-Provisional Utility Patent Application
        Application No.: To Be Assigned
        Filed: Herewith
        For: Nucleic Acid Molecules and Other Molecules
                        Associated with the Phosphogluconate Pathway
        Inventors: Nordine CHEIKH *et al.*
        Atty. Docket: 04983.0031.US01/38-21(15365)B

Sir:

The following documents are forwarded herewith for appropriate action by the U.S. Patent and Trademark Office:

1.   Utility Patent Application Transmittal (PTO/SB/05);

2.   U.S. Utility Patent Application entitled:

        Nucleic Acid Molecules and Other Molecules Associated with the Phosphogluconate Pathway

        and naming as inventors:

        Nordine Cheikh, Jingdong Liu, and Virginia M. Peschke

        the application consisting of:

        a.   A specification containing:

                (i)   _242_ pages of a description prior to the claims;

                (ii)   _5_ pages of claims (_9_ claims);

                (iii)   a one (1) page abstract; and

                (iv)   _237_ pages of a sequence listing;

3.   A computer readable disk copy of the sequence listing;

Washington, DC   Los Angeles   Silicon Valley

4.   Statement Regarding Sequence Submission; and

5.   Two (2) return postcards.

It is respectfully requested that, of the two attached postcards, one be stamped with the filing date of these documents and returned to our courier, and the other, prepaid postcard, be stamped with the filing date and unofficial application number and returned as soon as possible.

This application claims priority under 35 U.S.C §119(e) and/or 35 U.S.C §120 of applications No. 60/083,390, filed April 29, 1998, which is herein incorporated by reference in its entirety.

In accordance with 37 C.F.R. § 1.821(f), the paper copy of the sequence listing and the computer readable copy of the sequence listing submitted herewith in the above application are the same.

Respectfully submitted,

David R. Marsh (Reg. No. 41,408)

Enclosures

Please type a plus sign (+) inside this box ➔ | + |

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UTILITY PATENT APPLICATION TRANSMITTAL *(Only for new nonprovisional applications under 37 CFR 1.53(b))*	Attorney Docket No.	04983.0031.US01/38-21(15365)B	
	First Named Inventor or Application Identifier		CHEIKH
	Title	Nucleic Acid Molecules And Other Molecules Associated With the Phosphogluconate Pathway	
	Express Mail Label No.		

| **APPLICATION ELEMENTS** *See MPEP chapter 600 concerning utility patent application contents* | **ADDRESS TO:** Assistant Commissioner for Patents Box Patent Application Washington, DC 20231 |

1. ☐ *Fee Transmittal Form (Form PTO-1082) (Submit an original and a duplicate for fee processing)

2. ☒ Specification [*Total Pages* 248] *(preferred arrangement set forth below)*
- Descriptive title of the Invention
- Cross References to Related Applications
- Statement Regarding Fed sponsored R&D
- Reference to Microfiche Appendix
- Background of the Invention
- Brief Summary of the Invention
- Brief Description of the Drawings (if filed)
- Detailed Description
- Claims
- Abstract of the Disclosure

3. ☐ Drawing(s) (35 USC 113) [*Total Sheets*]

4. Oath or Declaration [*Total Pages*]
- a. ☐ Newly executed (original or copy)
- b. ☐ Copy from a prior application (37 CFR 1.63(d)) *(for continuation/divisional with Box 17 completed)* [*Note Box 5 below*]
  - i. ☐ DELETION OF INVENTOR(S) Signed statement attached deleting inventor(s) named in the prior application, see 37 CFR 1.63(d)(2) and 1.33(b).

5. ☐ Incorporation By Reference *(useable if Box 4b is checked)* The entire disclosure of the prior application, from which a copy of the oath or declaration is supplied under Box 4b, is considered as being part of the disclosure of the accompanying application and is hereby incorporated by reference therein.

6. ☐ Microfiche Computer Program *(Appendix)*

7. Nucleotide and/or Amino Acid Sequence Submission *(if applicable, all necessary)*
- a. ☒ Computer Readable Copy
- b. ☒ Paper Copy (identical to computer copy)
- c. ☒ Statement verifying identity of above copies

ACCOMPANYING APPLICATION PARTS

8. ☐ Assignment Papers (cover sheet & document(s))

9. ☐ 37 CFR 3.73(b) Statement *(when there is an assignee)* ☐ Power of Attorney

10. ☐ English Translation Document *(if applicable)*

11. ☐ Information Disclosure Statement (IDS)/PTO-1449 ☐ Copies of IDS Citations

12. ☐ Preliminary Amendment

13. ☒ Return Receipt Postcard (MPEP 503) (Two) *(should be specifically itemized)*

14. ☐ *Small Entity Statement(s) ☐ Statement filed in prior application, Status still proper and desired

15. ☐ Certified Copy of Priority Document(s) *(if foreign priority is claimed)*

16. ☐ Other:

*NOTE FOR ITEMS 1 & 14· IN ORDER TO BE ENTITLED TO PAY SMALL ENTITY FEES, A SMALL ENTITY STATEMENT IS REQUIRED (37 C.F.R. § 1 27), EXCEPT IF ONE FILED IN A PRIOR APPLICATION IS RELIED UPON (37 C.F.R. § 1.28).

17. If a CONTINUING APPLICATION, *check appropriate box and supply the requisite information:*
☐ Continuation ☐ Divisional ☐ Continuation-in-part (CIP) of prior application No: /
Prior Application Information: Examiner: Group/Art Unit:

18. CORRESPONDENCE ADDRESS

☐ *Customer Number or Bar Code Label* *(Insert Customer No. or Attach bar code label here)* or ☒ *Correspondence address below*

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Signature		Date	April 28, 1999	

NUCLEIC ACID MOLECULES AND OTHER MOLECULES ASSOCIATED WITH

THE PHOSPHOGLUCONATE PATHWAY

CROSS REFERENCE TO RELATED APPLICATIONS

This application claims priority under 35 U.S.C. § 119(e) to application serial no.

5   60/083,390, filed April 29, 1998, which is herein incorporated by reference in its entirety.

FIELD OF THE INVENTION

The present invention is in the field of plant biochemistry. More specifically the

invention relates to nucleic acid sequences from plant cells, in particular, nucleic acid sequences

from maize and soybean plants associated with the phosphogluconate pathway in plants. The

10   invention encompasses nucleic acid molecules that encode proteins and fragments of proteins. In

addition, the invention also encompasses proteins and fragments of proteins so encoded and

antibodies capable of binding these proteins or fragments. The invention also relates to methods

of using the nucleic acid molecules, proteins and fragments of proteins and antibodies, for

example for genome mapping, gene identification and analysis, plant breeding, preparation of

15   constructs for use in plant gene expression and transgenic plants.

BACKGROUND OF THE INVENTION

I.   PHOSPHOGLUCONATE PATHWAY

The phosphogluconate pathway (OPPP) (also known as the oxidative pentose phosphate

pathway, pentose phosphate shunt, or Warburg-Dickens pathway) is one of the two major

20   pathways in plants by which carbohydrates may be ultimately degraded into CO_2, the other being

glycolysis followed by the TCA cycle (Brownleader *et al.*, In: *Plant Biochemistry* Academic

Press, New York, pp. 111-141, (1997), the entirety of which is herein incorporated by reference).

It has been reported that the OPPP generally accounts for 10-15% of the carbohydrate oxidation

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in cells (apRees In: *The Biochemistry of Plants Vol 3*:1-42, (1980), the entirety of which is herein

incorporated by reference). It has been reported that the primary purposes of the OPPP is

production of NADPH for use in biosynthetic reactions and the production of a ribose-5-

phosphate for use in nucleic acid biosynthesis (Turner and Turner, In: *Biochemistry of Plants - A*

5   *Comprehensive Treatise Vol 2*:279-316, (1980), the entirety of which is herein incorporated by

reference). The subcellular localization of this pathway has been reported to differ between

species, cell type, and plastid type being investigated. For example, reported cellular

fractionation experiments in spinach leaf cells showed all enzymes of the phosphogluconate

pathway were found in chloroplasts, but that only the first two enzymes of that pathway are

10   present in the cytosol (Schnarrenberger *et al.*, *Plant Physiol. 108*:609-614, (1995), the entirety of

which is herein incorporated by reference).

In general, OPPP can be divided into two parts, oxidative (the reactions leading up to

ribulose-5-phosphate), and non-oxidative (*e.g.* Williams, *Trends Biochem. Sci. 5*:315-320,

(1980); apRees, In: *Encyclopedia of Plant Physiology Vol 18* pp.391-417, (1985), all of which

15   references are incorporated herein in their entirety).

The first reported reaction of OPPP is the conversion of glucose-6-phosphate by glucose-

6-phosphate dehydrogenase (G6PDH; EC 1.1.1.49) to 6-phosphogluconolactone. The hydrolysis

of 6-phosphogluconolactone to 6-phosphogluconate can occur in a nonenzymatically manner or

be catalyzed by a lactonase. This reaction is not at equilibrium and is irreversible (Ashihara and

20   Komamine, *Plant Sci. Lett. 2*:331-337 (1974), the entirety of which is herein incorporated by

reference; Turner and Turner, In: *Biochemistry of Plants - A Comprehensive Treatise Vol 2*:279-

316, (1980)). The hydrolysis of 6-phosphogluconolactone to 6-phosphogluconate is reported to

be a critical regulatory step in the phosphogluconate pathway. The hydrolysis of 6-

phosphogluconolactone to 6-phosphogluconate has been reported to respond to the concentration

of glucose-6-phosphate as well as the NADPH/NADP+ ratio. Inhibition of the hydrolysis of 6-

phosphogluconolactone to 6-phosphogluconate by NADPH is consistent with the function of

OPPP to provide NADPH (apRees, In: *The Biochemistry of Plants Vol 3*:1-42, (1980)). cDNA

5   clones for G6PDH have been isolated from several plants including alfalfa (Fahrendorf *et al.,*

Plant Mol. Biol. 28: 885-900, (1995), the entirety of which is herein incorporated by reference)

and potato (Graeve *et al., Plant J. 5*:353-361, (1994), the entirety of which is herein incorporated

by reference).

6-phosphogluconate is dehydrogenated to ribulose-5-phosphate, NADPH, and CO_2 in an

10   irreversible reaction catalyzed by 6-phosphogluconate dehydrogenase (6PGDH; EC1.1.1.44). A

cDNA clone for 6PGDH has been isolated from alfalfa (Fahrendorf *et al., Plant Mol Biol 28*:

885-900, (1995)). The first two steps of the OPPP are the only reported oxidation reactions in

that pathway. Other reactions within OPPP serve to regenerate glucose-6-phosphate, as well as

producing intermediates such as ribose-5-phosphate that are ultilized in nucleic acid biosynthesis.

15   Ribulose-5-phosphate may be metabolized in one of two pathways. Ribose-5-phosphate

isomerase (EC 5.3.1.6) catalyzes the conversion of ribulose-5-phosphate to ribose-5-phosphate,

while ribulose-5-phosphate-3-epimerase (also known as pentose-5-phosphate-3-epimerase; EC

5.1.3.1) catalyzes the conversion of ribulose-5-phosphate to xylulose-5-phosphate.

Transketolase (EC 2.2.1.1) catalyzes the conversion of ribulose-5-phosphate and xylulose-5-

20   phosphate into sedheptulose-7-phosphate and 3-phosphoglyceraldehyde. Transaldolase (EC

2.2.1.2) catalyzes the conversion of sedheptulose-7-phosphate and 3-phosphoglyceraldehyde into

erythrose-4-phosphate and fructose-6-phosphate.

Erythrose-4-phosphate is a substrate associated with the biosynthesis of lignin (Salisbury and Ross, *Plant Physiology,* Wadsworth Publishing Company, Belmont CA, (1978), the entirety of which is herein incorporated by reference), or the production of aromatic amino acids via the shikimate pathway (Schnarrenberger *et al., Plant Physiol. 108*:609-614, (1995), the entirety of

5   which is herein incorporated by reference). Clones for potato transaldolase (Moehs *et al., Plant Mol. Biol. 32*:447-452, (1996), the entirety of which is herein incorporated by reference); spinach transketolase (Flechner *et al., Plant Mol. Biol. 32*:475-484, (1996), the entirety of which is herein incorporated by reference); potato ribulose-5-phosphate-3-epimerase (Teige *et al., FEBS Lett.* 377:349-352, (1995), the entirety of which is herein incorporated by reference); and spinach

10   ribulose-5-phosphate-3-epimerase (Nowitzki *et al., Plant Mol. Biol. 29*:1279-1291, (1995), the entirety of which is herein incorporated by reference) have been reported.

Fructose-6-phosphate may enter glycolysis (apRees, In: *The Biochemistry of Plants Vol 3*:1-42, (1980)). Fructose-6-phosphate can also be converted to glucose-6-phosphate via phosphohexose isomerase (also known as phosphoglucoisomerase)(EC5.3.1.9). Glucose-6-

15   phosphate can be recycled in the OPPP pathway or be utilized during the synthesis of polysaccharides.

Transketolase (EC2.2.1.1) can catalyze the conversion of erythrose-4-phosphate and xylulose-5-phosphate to fructose 6-phosphate and 3-phosphoglyceraledehyde. Likewise, fructose 6-phosphate and 3-phosphoglyceraledehyde may be used in reactions as described

20   above.

II.   EXPRESSED SEQUENCE TAG NUCLEIC ACID MOLECULES

Expressed sequence tags, or ESTs are randomly sequenced members of a cDNA library (or complementary DNA)(McCombie *et al., Nature Genetics 1:*124-130 (1992); Kurata *et al.,*

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Nature Genetics 8: 365-372 (1994); Okubo, *et al. Nature Genetics 2:* 173-179 (1992), all of

which references are incorporated herein in their entirety). The randomly selected clones

comprise insets that can represent a copy of up to the full length of a mRNA transcript.

Using conventional methodologies, cDNA libraries can be constructed from the mRNA

5   (messenger RNA) of a given tissue or organism using poly dT primers and reverse transcriptase

(Efstratiadis *et al., Cell 7:*279-288 (1976), the entirety of which is herein incorporated by

reference; Higuchi *et al., Proc. Natl. Acad. Sci. (U.S.A.) 73:*3146-3150 (1976), the entirety of

which is herein incorporated by reference; Maniatis *et al., Cell 8:*163-182 (1976) the entirety of

which is herein incorporated by reference; Land *et al., Nucleic Acids Res. 9:*2251-2266 (1981),

10   the entirety of which is herein incorporated by reference; Okayama *et al., Mol. Cell. Biol. 2:*161-

170 (1982), the entirety of which is herein incorporated by reference; Gubler *et al., Gene 25:*263-

269 (1983), the entirety of which is herein incorporated by reference).

Several methods may be employed to obtain full-length cDNA constructs. For example,

terminal transferase can be used to add homopolymeric tails of dC residues to the free 3'

15   hydroxyl groups (Land *et al., Nucleic Acids Res. 9:*2251-2266 (1981), the entirety of which is

herein incorporated by reference). This tail can then be hybridized by a poly dG oligo which can

act as a primer for the synthesis of full length second strand cDNA. Okayama and Berg, *Mol.*

Cell. Biol. 2: 161-170 (1982), the entirety of which is herein incorporated by reference, report a

method for obtaining full length cDNA constructs. This method has been simplified by using

20   synthetic primer-adapters that have both homopolymeric tails for priming the synthesis of the

first and second strands and restriction sites for cloning into plasmids (Coleclough *et al., Gene*

*34:*305-314 (1985), the entirety of which is herein incorporated by reference) and bacteriophage

vectors (Krawinkel *et al., Nucleic Acids Res. 14:*1913 (1986), the entirety of which is herein

incorporated by reference; Han *et al.*, *Nucleic Acids Res. 15*:6304 (1987), the entirety of which is herein incorporated by reference).

These strategies have been coupled with additional strategies for isolating rare mRNA populations. For example, a typical mammalian cell contains between 10,000 and 30,000 different mRNA sequences (Davidson, *Gene Activity in Early Development*, 2nd ed., Academic Press, New York (1976). The number of clones required to achieve a given probability that a low-abundance mRNA will be present in a cDNA library is $N = (\ln(1-P))/(\ln(1-1/n))$ where N is the number of clones required, P is the probability desired, and 1/n is the fractional proportion of the total mRNA that is represented by a single rare mRNA (Sambrook *et al.*, *Molecular Cloning: A Laboratory Manual*, 2nd ed., Cold Spring Harbor Laboratory Press (1989), the entirety of which is herein incorporated by reference).

A method to enrich preparations of mRNA for sequences of interest is to fractionate by size. One such method is to fractionate by electrophoresis through an agarose gel (Pennica *et al.*, *Nature 301*:214-221 (1983), the entirety of which is herein incorporated by reference). Another such method employs sucrose gradient centrifugation in the presence of an agent, such as methylmercuric hydroxide, that denatures secondary structure in RNA (Schweinfest *et al.*, *Proc. Natl. Acad. Sci. (U.S.A.) 79*:4997-5000 (1982), the entirety of which is herein incorporated by reference).

A frequently adopted method is to construct equalized or normalized cDNA libraries (Ko, *Nucleic Acids Res. 18*:5705-5711 (1990), the entirety of which is herein incorporated by reference; Patanjali, S. R. *et al.*, *Proc. Natl. Acad. Sci. (U.S.A.) 88*:1943-1947 (1991), the entirety of which is herein incorporated by reference). Typically, the cDNA population is normalized by subtractive hybridization (Schmid *et al.*, *J. Neurochem. 48*:307-312 (1987) the entirety of which

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is herein incorporated by reference; Fargnoli *et al.*, *Anal. Biochem.* *187*:364-373 (1990) the

entirety of which is herein incorporated by reference; Travis *et al.*, *Proc. Natl. Acad. Sci (U.S.A.)*

85:1696-1700 (1988) the entirety of which is herein incorporated by reference; Kato, *Eur. J.*

Neurosci. *2*:704-711 (1990); and Schweinfest *et al.*, *Genet. Anal. Tech. Appl.* *7*:64-70 (1990), the

5   entirety of which is herein incorporated by reference). Subtraction represents another method for

reducing the population of certain sequences in the cDNA library (Swaroop *et al.*, *Nucleic Acids*

Res. *19*:1954 (1991), the entirety of which is herein incorporated by reference).

ESTs can be sequenced by a number of methods. Two basic methods may be used for

DNA sequencing, the chain termination method of Sanger *et al.*, *Proc. Natl. Acad. Sci. (U.S.A.)*

10   *74:* 5463-5467 (1977), the entirety of which is herein incorporated by reference, and the

chemical degradation method of Maxam and Gilbert, *Proc. Nat. Acad. Sci. (U.S.A.) 74:* 560-564

(1977), the entirety of which is herein incorporated by reference. Automation and advances in

technology such as the replacement of radioisotopes with fluorescence-based sequencing have

reduced the effort required to sequence DNA (Craxton, *Methods 2:* 20-26 (1991), the entirety of

15   which is herein incorporated by reference; Ju *et al.*, *Proc. Natl. Acad. Sci. (U.S.A.) 92:* 4347-

4351 (1995), the entirety of which is herein incorporated by reference; Tabor and Richardson,

Proc. Natl. Acad. Sci. (U.S.A.) 92: 6339-6343 (1995), the entirety of which is herein incorporated

by reference). Automated sequencers are available from, for example, Pharmacia Biotech, Inc.,

Piscataway, New Jersey (Pharmacia ALF), LI-COR, Inc., Lincoln, Nebraska (LI-COR 4,000)

20   and Millipore, Bedford, Massachusetts (Millipore BaseStation).

In addition, advances in capillary gel electrophoresis have also reduced the effort required

to sequence DNA and such advances provide a rapid high resolution approach for sequencing

DNA samples (Swerdlow and Gesteland, *Nucleic Acids Res.* *18*:1415-1419 (1990); Smith,

Nature 349:812-813 (1991); Luckey *et al., Methods Enzymol. 218*:154-172 (1993); Lu *et al., J. Chromatog. A. 680*:497-501 (1994); Carson *et al., Anal. Chem. 65*:3219-3226 (1993); Huang *et al., Anal. Chem 64*:2149-2154 (1992); Kheterpal *et al., Electrophoresis 17*:1852-1859 (1996); Quesada and Zhang, *Electrophoresis 17*:1841-1851 (1996); Baba, *Yakugaku Zasshi 117*:265-281 (1997), all of which are herein incorporated by reference in their entirety).

ESTs longer than 150 nucleotides have been found to be useful for similarity searches and mapping (Adams *et al., Science 252*:1651-1656 (1991), herein incorporated by reference). ESTs, which can represent copies of up to the full length transcript, may be partially or completely sequenced. Between 150-450 nucleotides of sequence information is usually generated as this is length of sequence information that is routinely and reliably produced using single run sequence data. Typically, only single run sequence data is obtained from the cDNA library (Adams *et al., Science 252*:1651-1656 (1991). Automated single run sequencing typically results in an approximately 2-3% error or base ambiguity rate (Boguski *et al., Nature Genetics 4*:332-333 (1993), the entirety of which is herein incorporated by reference).

EST databases have been constructed or partially constructed from, for example, *C. elegans* (McCombrie *et al., Nature Genetics 1*:124-131 (1992)), human liver cell line HepG2 (Okubo *et al., Nature Genetics 2*:173-179 (1992)), human brain RNA (Adams *et al., Science 252*:1651-1656 (1991)); Adams *et al., Nature 355*:632-635 (1992)), *Arabidopsis,* (Newman *et al., Plant Physiol. 106*:1241-1255 (1994)); and rice (Kurata *et al., Nature Genetics 8*:365-372 (1994)).

III.   SEQUENCE COMPARISONS

A characteristic feature of a protein or DNA sequence is that it can be compared with other known protein or DNA sequences. Sequence comparisons can be undertaken by

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determining the similarity of the test or query sequence with sequences in publicly available or

proprietary databases ("similarity analysis") or by searching for certain motifs ("intrinsic

sequence analysis")(e.g. *cis* elements)(Coulson, *Trends in Biotechnology 12:* 76-80 (1994), the

entirety of which is herein incorporated by reference); Birren *et al., Genome Analysis 1:* Cold

5   Spring Harbor Laboratory Press, Cold Spring Harbor, New York 543-559 (1997), the entirety of

which is herein incorporated by reference).

Similarity analysis includes database search and alignment. Examples of public

databases include the DNA Database of Japan (DDBJ)(http://www.ddbj.nig.ac.jp/); Genebank

(http://www.ncbi.nlm.nih.gov/Web/Search/Index.htlm); and the European Molecular Biology

10   Laboratory Nucleic Acid Sequence Database (EMBL)

(http://www.ebi.ac.uk/ebi_docs/embl_db/embl-db.html). A number of different search

algorithms have been developed, one example of which are the suite of programs referred to as

BLAST programs. There are five implementations of BLAST, three designed for nucleotide

sequences queries (BLASTN, BLASTX, and TBLASTX) and two designed for protein sequence

15   queries (BLASTP and TBLASTN) (Coulson, *Trends in Biotechnology 12:* 76-80 (1994); Birren

et al., Genome Analysis 1: Cold Spring Harbor Laboratory Press, Cold Spring Harbor, New York

543-559 (1997)).

BLASTN takes a nucleotide sequence (the query sequence) and its reverse complement

and searches them against a nucleotide sequence database. BLASTN was designed for speed,

20   not maximum sensitivity, and may not find distantly related coding sequences. BLASTX takes a

nucleotide sequence, translates it in three forward reading frames and three reverse complement

reading frames, and then compares the six translations against a protein sequence database.

BLASTX is useful for sensitive analysis of preliminary (single-pass) sequence data and is

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tolerant of sequencing errors (Gish and States, *Nature Genetics 3:* 266-272 (1993), the entirety of which is herein incorporated by reference). BLASTN and BLASTX may be used in concert for analyzing EST data (Coulson, *Trends in Biotechnology 12:* 76-80 (1994); Birren *et al., Genome Analysis 1:* 543-559 (1997)).

5   Given a coding nucleotide sequence and the protein it encodes, it is often preferable to use the protein as the query sequence to search a database because of the greatly increased sensitivity to detect more subtle relationships. This is due to the larger alphabet of proteins (20 amino acids) compared with the alphabet of nucleic acid sequences (4 bases), where it is far easier to obtain a match by chance. In addition, with nucleotide alignments, only a match

10   (positive score) or a mismatch (negative score) is obtained, but with proteins, the presence of conservative amino acid substitutions can be taken into account. Here, a mismatch may yield a positive score if the non-identical residue has physical/chemical properties similar to the one it replaced. Various scoring matrices are used to supply the substitution scores of all possible amino acid pairs. A general purpose scoring system is the BLOSUM62 matrix (Henikoff and

15   Henikoff, *Proteins 17:* 49-61 (1993), the entirety of which is herein incorporated by reference), which is currently the default choice for BLAST programs. BLOSUM62 is tailored for alignments of moderately diverged sequences and thus may not yield the best results under all conditions. Altschul, *J. Mol. Biol. 36:* 290-300 (1993), the entirety of which is herein incorporated by reference, describes a combination of three matrices to cover all contingencies.

20   This may improve sensitivity, but at the expense of slower searches. In practice, a single BLOSUM62 matrix is often used but others (PAM40 and PAM250) may be attempted when additional analysis is necessary. Low PAM matrices are directed at detecting very strong but

localized sequence similarities, whereas high PAM matrices are directed at detecting long but weak alignments between very distantly related sequences.

Homologues in other organisms are available that can be used for comparative sequence analysis. Multiple alignments are performed to study similarities and differences in a group of related sequences. CLUSTAL W is a multiple sequence alignment package that performs progressive multiple sequence alignments based on the method of Feng and Doolittle, *J. Mol. Evol.* 25: 351-360 (1987), the entirety of which is herein incorporated by reference. Each pair of sequences is aligned and the distance between each pair is calculated; from this distance matrix, a guide tree is calculated, and all of the sequences are progressively aligned based on this tree. A feature of the program is its sensitivity to the effect of gaps on the alignment; gap penalties are varied to encourage the insertion of gaps in probable loop regions instead of in the middle of structured regions. Users can specify gap penalties, choose between a number of scoring matrices, or supply their own scoring matrix for both pairwise alignments and multiple alignments. CLUSTAL W for UNIX and VMS systems is available at: ftp.ebi.ac.uk. Another program is MACAW (Schuler *et al.*, *Proteins Struct. Func. Genet. 9:*180-190 (1991), the entirety of which is herein incorporated by reference, for which both Macintosh and Microsoft Windows versions are available. MACAW uses a graphical interface, provides a choice of several alignment algorithms, and is available by anonymous ftp at: ncbi.nlm.nih.gov (directory/pub/macaw).

Sequence motifs are derived from multiple alignments and can be used to examine individual sequences or an entire database for subtle patterns. With motifs, it is sometimes possible to detect distant relationships that may not be demonstrable based on comparisons of primary sequences alone. Currently, the largest collection of sequence motifs in the world is

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PROSITE (Bairoch and Bucher, *Nucleic Acid Research 22:* 3583-3589 (1994), the entirety of which is herein incorporated by reference). PROSITE may be accessed via either the ExPASy server on the World Wide Web or anonymous ftp site. Many commercial sequence analysis packages also provide search programs that use PROSITE data.

5   A resource for searching protein motifs is the BLOCKS E-mail server developed by S. Henikoff, *Trends Biochem Sci. 18:*267-268 (1993), the entirety of which is herein incorporated by reference; Henikoff and Henikoff, *Nucleic Acid Research 19:*6565-6572 (1991), the entirety of which is herein incorporated by reference; Henikoff and Henikoff, *Proteins, 17:* 49-61 (1993). BLOCKS searches a protein or nucleotide sequence against a database of protein motifs or

10   "blocks." Blocks are defined as short, ungapped multiple alignments that represent highly conserved protein patterns. The blocks themselves are derived from entries in PROSITE as well as other sources. Either a protein query or a nucleotide query can be submitted to the BLOCKS server; if a nucleotide sequence is submitted, the sequence is translated in all six reading frames and motifs are sought for these conceptual translations. Once the search is completed, the server

15   will return a ranked list of significant matches, along with an alignment of the query sequence to the matched BLOCKS entries.

Conserved protein domains can be represented by two-dimensional matrices, which measure either the frequency or probability of the occurrences of each amino acid residue and deletions or insertions in each position of the domain. This type of model, when used to search

20   against protein databases, is sensitive and usually yields more accurate results than simple motif searches. Two popular implementations of this approach are profile searches (such as GCG program ProfileSearch) and Hidden Markov Models (HMMs)(Krough. *et al., J. Mol. Biol. 235:*1501-1531, (1994); Eddy, *Current Opinion in Structural Biology, 6:*361-365, (1996), both of

which are herein incorporated by reference in their entirety). In both cases, a large number of

common protein domains have been converted into profiles, as present in the PROSITE library,

or HHM models, as in the Pfam protein domain library (Sonnhammer *et al., Proteins 28*:405-420

(1997), the entirety of which is herein incorporated by reference). Pfam contains more than 500

5   HMM models for enzymes, transcription factors, signal transduction molecules, and structural

proteins. Protein databases can be queried with these profiles or HMM models, which will

identify proteins containing the domain of interest. For example, HMMSW or HMMFS, two

programs in a public domain package called HMMER (Sonnhammer *et al., Proteins 28*:405-420,

(1997)) can be used.

10   PROSITE and BLOCKS represent collected families of protein motifs. Thus, searching

these databases entails submitting a single sequence to determine whether or not that sequence is

similar to the members of an established family. Programs working in the opposite direction

compare a collection of sequences with individual entries in the protein databases. An example

of such a program is the Motif Search Tool, or MoST (Tatusov *et al. Proc. Natl. Acad. Sci. 91:*

15   12091-12095 (1994), the entirety of which is herein incorporated by reference). On the basis of

an aligned set of input sequences, a weight matrix is calculated by using one of four methods

(selected by the user). A weight matrix is simply a representation, position by position of how

likely a particular amino acid will appear. The calculated weight matrix is then used to search

the databases. To increase sensitivity, newly found sequences are added to the original data set,

20   the weight matrix is recalculated, and the search is performed again. This procedure continues

until no new sequences are found.

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SUMMARY OF THE INVENTION

The present invention provides a substantially purified nucleic acid molecule that encodes a maize or soybean phosphogluconate pathway enzyme or fragment thereof, wherein the maize or soybean phosphogluconate pathway enzyme is selected from the group consisting of: (a) glucose-6-phosphate-1-dehydrogenase; (b) 6-phosphogluconate dehydrogenase; (c) putative 6-phosphogluconate dehydrogenase; (d) D-ribulose-5-phosphate-3-epimerase; (e) ribose-5-phosphate isomerase; (f) putative ribose-5-phosphate isomerase; (g) transketolase; (h) putative transketolase; (i) transaldolase; (j) putative transaldolase; and (k) phosphoglucoisomerase.

The present invention also provides a substantially purified nucleic acid molecule that encodes a plant phosphogluconate pathway enzyme or fragment thereof, wherein the nucleic acid molecule is selected from the group consisting of a nucleic acid molecule that encodes a maize or soybean glucose-6-phosphate-1-dehydrogenase enzyme or fragment thereof; a nucleic acid molecule that encodes a maize or soybean 6-phosphogluconate dehydrogenase enzyme or fragment thereof; a nucleic acid molecule that encodes a putative maize or soybean 6-phosphogluconate dehydrogenase enzyme or fragment thereof; a nucleic acid molecule that encodes a maize or soybean D-ribulose-5-phosphate-3-epimerase enzyme or fragment thereof; a nucleic acid molecule that encodes a maize or soybean ribose-5-phosphate isomerase enzyme or fragment thereof; a nucleic acid molecule that encodes a putative maize or soybean ribose-5-phosphate isomerase enzyme or fragment thereof; a nucleic acid molecule that encodes a maize or soybean transketolase enzyme or fragment thereof; a nucleic acid molecule that encodes a putative maize or soybean transketolase enzyme or fragment thereof; a nucleic acid molecule that encodes a maize or soybean transaldolase enzyme or fragment thereof; a nucleic acid molecule

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that encodes a maize putative transaldolase enzyme or fragment thereof; and a nucleic acid molecule that encodes a maize or soybean phosphoglucoisomerase enzyme or fragment thereof.

The present invention also provides a substantially purified maize or soybean phosphogluconate pathway enzyme or fragment thereof, wherein the maize or soybean phosphogluconate pathway enzyme is selected from the group consisting of (a) glucose-6-phosphate-1-dehydrogenase or fragment thereof; (b) 6-phosphogluconate dehydrogenase or fragment thereof; (c) putative 6-phosphogluconate dehydrogenase or fragment thereof; (d) D-ribulose-5-phosphate-3-epimerase or fragment thereof; (e) ribose-5-phosphate isomerase or fragment thereof; (f) putative ribose-5-phosphate isomerase or fragment thereof; (g) transketolase or fragment thereof; (h) putative transketolase or fragment thereof; (i) transaldolase or fragment thereof; (j) putative transaldolase or fragment thereof; and (k) phosphoglucoisomerase or fragment thereof.

The present invention also provides a substantially purified maize or soybean phosphogluconate pathway enzyme or fragment thereof encoded by a first nucleic acid molecule which specifically hybridizes to a second nucleic acid molecule, the second nucleic acid molecule having a nucleic acid sequence selected from the group consisting of a complement of SEQ ID NO: 1 through SEQ ID NO: 699.

The present invention also provides a substantially purified maize or soybean glucose-6-phosphate-1-dehydrogenase enzyme or fragment thereof encoded by a first nucleic acid molecule which specifically hybridizes to a second nucleic acid molecule, the second nucleic acid molecule having a nucleic acid sequence selected from the group consisting of a complement of SEQ ID NO: 1 through SEQ ID NO: 3 and SEQ ID NO: 4 through SEQ ID NO: 11.

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The present invention also provides a substantially purified maize or soybean glucose-6-phosphate-1-dehydrogenase enzyme or fragment thereof encoded by a nucleic acid sequence selected from the group consisting of SEQ ID NO: 1 through SEQ ID NO: 3 and SEQ ID NO: 4 through SEQ ID NO: 11.

5   The present invention also provides a substantially purified maize or soybean 6-phosphogluconate dehydrogenase enzyme or fragment thereof encoded by a first nucleic acid molecule which specifically hybridizes to a second nucleic acid molecule, the second nucleic acid molecule having a nucleic acid sequence selected from the group consisting of a complement of SEQ ID NO: 12 through SEQ ID NO: 21 and SEQ ID NO: 22 through SEQ ID NO: 103.

10   The present invention also provides a substantially purified maize or soybean 6-phosphogluconate dehydrogenase enzyme or fragment thereof encoded by a nucleic acid sequence selected from the group consisting of SEQ ID NO: 12 through SEQ ID NO:21 and SEQ ID NO: 22 through SEQ ID NO: 103.

15   The present invention also provides a substantially purified putative maize or soybean 6-phosphogluconate dehydrogenase enzyme or fragment thereof enzyme or fragment thereof encoded by a first nucleic acid molecule which specifically hybridizes to a second nucleic acid molecule, the second nucleic acid molecule having a nucleic acid sequence of a complement of SEQ ID NO: 104 through SEQ ID NO: 209 and SEQ ID NO: 210 through SEQ ID NO: 214.

20   The present invention also provides a substantially purified putative maize or soybean 6-phosphogluconate dehydrogenase enzyme or fragment thereof encoded by a nucleic acid sequence of SEQ ID NO: 104 through SEQ ID NO: 209 and SEQ ID NO: 210 through SEQ ID NO: 214.

The present invention also provides a substantially purified maize or soybean D-ribulose-5-phosphate-3-epimerase enzyme or fragment thereof encoded by a first nucleic acid molecule which specifically hybridizes to a second nucleic acid molecule, the second nucleic acid molecule having a nucleic acid sequence selected from the group consisting of a complement of

5   SEQ ID NO: 215 through SEQ ID NO: 260 and SEQ ID NO: 261 through SEQ ID NO: 299.

The present invention also provides a substantially purified maize or soybean D-ribulose-5-phosphate-3-epimerase enzyme or fragment thereof encoded by a nucleic acid sequence selected from the group consisting of SEQ ID NO: 215 through SEQ ID NO: 260 and SEQ ID NO: 261 through SEQ ID NO: 299.

10   The present invention also provides a substantially purified maize or soybean ribose-5-phosphate isomerase enzyme or fragment thereof encoded by a first nucleic acid molecule which specifically hybridizes to a second nucleic acid molecule, the second nucleic acid molecule having a nucleic acid sequence selected from the group consisting of a complement of SEQ ID NO: 300 through SEQ ID NO: 306 and SEQ ID NO: 307 through SEQ ID NO: 311.

15   The present invention also provides a substantially purified maize or soybean ribose-5-phosphate isomerase enzyme or fragment thereof encoded by a nucleic acid sequence selected from the group consisting of SEQ ID NO: 300 through SEQ ID NO: 306 and SEQ ID NO: 307 through SEQ ID NO: 311.

The present invention also provides a substantially purified putative maize or soybean

20   ribose-5-phosphate isomerase enzyme or fragment thereof encoded by a first nucleic acid molecule which specifically hybridizes to a second nucleic acid molecule, the second nucleic acid molecule having a nucleic acid sequence selected from the group consisting of a

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complement of SEQ ID NO: 312 through SEQ ID NO: 313 and SEQ ID NO: 314 through SEQ ID NO: 318.

The present invention also provides a substantially purified putative maize or soybean ribose-5-phosphate isomerase enzyme or fragment thereof encoded by a nucleic acid sequence selected from the group consisting of SEQ ID NO: 312 through SEQ ID NO: 313 and SEQ ID NO: 314 through SEQ ID NO: 318.

The present invention also provides a substantially purified maize or soybean transketolase enzyme or fragment thereof encoded by a first nucleic acid molecule which specifically hybridizes to a second nucleic acid molecule, the second nucleic acid molecule having a nucleic acid sequence selected from the group consisting of a complement of SEQ ID NO: 319 through SEQ ID NO: 356 and SEQ ID NO: 357 through SEQ ID NO: 437.

The present invention also provides a substantially purified maize or soybean transketolase enzyme or fragment thereof encoded by a nucleic acid sequence selected from the group consisting of SEQ ID NO: 319 through SEQ ID NO: 356 and SEQ ID NO: 357 through SEQ ID NO: 437.

The present invention also provides a substantially purified putative maize or soybean transketolase enzyme or fragment thereof encoded by a first nucleic acid molecule which specifically hybridizes to a second nucleic acid molecule, the second nucleic acid molecule having a nucleic acid sequence selected from the group consisting of a complement of SEQ ID NO: 438 through SEQ ID NO: 447 and SEQ ID NO: 448 through SEQ ID NO: 453.

The present invention also provides a substantially purified putative maize or soybean transketolase enzyme or fragment thereof encoded by a nucleic acid sequence selected from the

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group consisting of SEQ ID NO: 438 through SEQ ID NO: 447 and SEQ ID NO: 448 through SEQ ID NO: 453.

The present invention also provides a substantially purified maize or soybean transaldolase enzyme or fragment thereof encoded by a first nucleic acid molecule which

5   specifically hybridizes to a second nucleic acid molecule, the second nucleic acid molecule having a nucleic acid sequence selected from the group consisting of a complement of SEQ ID NO: 454 through SEQ ID NO: 533 and SEQ ID NO: 534 through SEQ ID NO: 617.

The present invention also provides a substantially purified maize or soybean transaldolase enzyme or fragment thereof encoded by a nucleic acid sequence selected from the

10   group consisting of of SEQ ID NO: 454 through SEQ ID NO: 533 and SEQ ID NO: 534 through SEQ ID NO: 617.

The present invention also provides a substantially purified putative maize transaldolase enzyme or fragment thereof encoded by a first nucleic acid molecule which specifically hybridizes to a second nucleic acid molecule, the second nucleic acid molecule having a nucleic

15   acid sequence selected from the group consisting of a complement of SEQ ID NO: 618.

The present invention also provides a substantially purified putative maize transaldolase enzyme or fragment thereof encoded by a nucleic acid sequence selected from the group consisting of SEQ ID NO: 618.

The present invention also provides a substantially purified maize or soybean

20   phosphoglucoisomerase enzyme or fragment thereof encoded by a first nucleic acid molecule which specifically hybridizes to a second nucleic acid molecule, the second nucleic acid molecule having a nucleic acid sequence selected from the group consisting of a complement of SEQ ID NO: 619 through SEQ ID NO: 683 and SEQ ID NO: 684 through SEQ ID NO: 699.

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The present invention also provides a substantially purified maize or soybean phosphoglucoisomerase enzyme or fragment thereof encoded by a nucleic acid sequence selected from the group consisting of SEQ ID NO: 619 through SEQ ID NO: 683 and SEQ ID NO: 684 through SEQ ID NO: 699.

5   The present invention also provides a purified antibody or fragment thereof which is capable of specifically binding to a maize or soybean phosphogluconate pathway enzyme or fragment thereof, wherein the maize or soybean phosphogluconate pathway enzyme or fragment thereof is encoded by a nucleic acid molecule comprising a nucleic acid sequence selected from the group consisting of SEQ ID NO: 1 through SEQ ID NO: 699.

10   The present invention also provides a substantially purified antibody or fragment thereof, the antibody or fragment thereof capable of specifically binding to a substantially purified maize or soybean glucose-6-phosphate-1-dehydrogenase enzyme or fragment thereof encoded by a first nucleic acid molecule which specifically hybridizes to a second nucleic acid molecule, the second nucleic acid molecule having a nucleic acid sequence selected from the group consisting of a complement of SEQ ID NO: 1 through SEQ ID NO: 3 and SEQ ID NO: 4 through SEQ ID NO: 11.

The present invention also provides a substantially purified antibody or fragment thereof, the antibody or fragment thereof capable of specifically binding to a maize or soybean 6-phosphogluconate dehydrogenase enzyme or fragment thereof encoded by a first nucleic acid

20   molecule which specifically hybridizes to a second nucleic acid molecule, the second nucleic acid molecule having a nucleic acid sequence consisting of a complement of SEQ ID NO: 12 through SEQ ID NO: 21 and SEQ ID NO: 22 through SEQ ID NO: 103.

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The present invention also provides a substantially purified antibody or fragment thereof, the antibody or fragment thereof capable of specifically binding to a putative maize or soybean 6-phosphogluconate dehydrogenase enzyme or fragment thereof enzyme or fragment thereof encoded by a first nucleic acid molecule which specifically hybridizes to a second nucleic acid

5   molecule, the second nucleic acid molecule having a nucleic acid sequence selected from the group consisting of a complement of SEQ ID NO: 104 through SEQ ID NO: 209 and SEQ ID NO: 210 through SEQ ID NO: 214.

The present invention also provides a substantially purified antibody or fragment thereof, the antibody or fragment thereof capable of specifically binding to a maize or soybean D-

10   ribulose-5-phosphate-3-epimerase enzyme or fragment thereof encoded by a first nucleic acid molecule which specifically hybridizes to a second nucleic acid molecule, the second nucleic acid molecule having a nucleic acid sequence selected from the group consisting of a complement of SEQ ID NO: 215 through SEQ ID NO: 260 and SEQ ID NO: 261 through SEQ ID NO: 299.

15   The present invention also provides a substantially purified antibody or fragment thereof, the antibody or fragment thereof capable of specifically binding to a maize or soybean ribose-5-phosphate isomerase enzyme or fragment thereof encoded by a first nucleic acid molecule which specifically hybridizes to a second nucleic acid molecule, the second nucleic acid molecule having a nucleic acid sequence selected from the group consisting of a complement of SEQ ID

20   NO: 300 through SEQ ID NO: 306 and SEQ ID NO: 307 through SEQ ID NO: 311.

The present invention also provides a substantially purified antibody or fragment thereof, the antibody or fragment thereof capable of specifically binding to a putative maize or soybean ribose-5-phosphate isomerase enzyme or fragment thereof encoded by a first nucleic acid

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molecule which specifically hybridizes to a second nucleic acid molecule, the second nucleic acid molecule having a nucleic acid sequence selected from the group consisting of a complement of SEQ ID NO: 312 through SEQ ID NO: 313 and SEQ ID NO: 314 through SEQ ID NO: 318.

5   The present invention also provides a substantially purified antibody or fragment thereof, the antibody or fragment thereof capable of specifically binding to a maize or soybean transketolase enzyme or fragment thereof encoded by a first nucleic acid molecule which specifically hybridizes to a second nucleic acid molecule, the second nucleic acid molecule having a nucleic acid sequence selected from the group consisting of a complement of SEQ ID NO: 319 through SEQ ID NO: 356 and SEQ ID NO: 357 through SEQ ID NO: 437.

The present invention also provides a substantially purified antibody or fragment thereof, the antibody or fragment thereof capable of specifically binding to a putative maize or soybean transketolase enzyme or fragment thereof encoded by a first nucleic acid molecule which specifically hybridizes to a second nucleic acid molecule, the second nucleic acid molecule having a nucleic acid sequence selected from the group consisting of a complement of SEQ ID NO: 438 through SEQ ID NO: 447 and SEQ ID NO: 448 through SEQ ID NO: 453.

The present invention also provides a substantially purified antibody or fragment thereof, the antibody or fragment thereof capable of specifically binding to a maize or soybean transaldolase enzyme or fragment thereof encoded by a first nucleic acid molecule which

20   specifically hybridizes to a second nucleic acid molecule, the second nucleic acid molecule having a nucleic acid sequence selected from the group consisting of a complement of SEQ ID NO: 454 through SEQ ID NO: 533 and SEQ ID NO: 534 through SEQ ID NO: 617.

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The present invention also provides a substantially purified antibody or fragment thereof, the antibody or fragment thereof capable of specifically binding to a putative maize transaldolase enzyme or fragment thereof encoded by a first nucleic acid molecule which specifically hybridizes to a second nucleic acid molecule, the second nucleic acid molecule having a nucleic

5   acid sequence consisting of a complement of SEQ ID NO: 618.

The present invention also provides a substantially purified antibody or fragment thereof, the antibody or fragment thereof capable of specifically binding to a maize or soybean phosphoglucoisomerase enzyme or fragment thereof encoded by a first nucleic acid molecule which specifically hybridizes to a second nucleic acid molecule, the second nucleic acid

10   molecule having a nucleic acid sequence selected from the group consisting of a complement of SEQ ID NO: 619 through SEQ ID NO: 683 and SEQ ID NO: 684 through SEQ ID NO: 699.

The present invention also provides a transformed plant having a nucleic acid molecule which comprises: (A) an exogenous promoter region which functions in a plant cell to cause the production of a mRNA molecule; (B) a structural nucleic acid molecule comprising a nucleic

15   acid sequence selected from the group consisting of (a) a nucleic acid sequence which encodes for a glucose-6-phosphate-1-dehydrogenase enzyme or fragment thereof; (b) a nucleic acid sequence which encodes for a 6-phosphogluconate dehydrogenase enzyme or fragment thereof; (c) a nucleic acid sequence which encodes for a putative 6-phosphogluconate dehydrogenase enzyme or fragment thereof; (d) a nucleic acid sequence which encodes for a D-ribulose-5-

20   phosphate-3-epimerase enzyme or fragment thereof; (e) a nucleic acid sequence which encodes for a ribose-5-phosphate isomerase enzyme or fragment thereof; (f) a nucleic acid sequence which encodes for a putative ribose-5-phosphate isomerase enzyme or fragment thereof; (g) a nucleic acid sequence which encodes for a transketolase enzyme or fragment thereof; (h) a

nucleic acid sequence which encodes for a putative transketolase enzyme or fragment thereof; (i) a nucleic acid sequence which encodes for a transaldolase enzyme or fragment thereof; (j) a nucleic acid sequence which encodes for a putative transaldolase enzyme or fragment thereof; (k) a nucleic acid sequence which encodes for a phosphoglucoisomerase enzyme or fragment thereof

5   and (l) a nucleic acid sequence which is complementary to any of the nucleic acid sequences of (a) through (k); and (C) a 3' non-translated sequence that functions in the plant cell to cause termination of transcription and addition of polyadenylated ribonucleotides to a 3' end of the mRNA molecule.

The present invention also provides a transformed plant having a nucleic acid molecule

10   which comprises: (A) an exogenous promoter region which functions in a plant cell to cause the production of a mRNA molecule; which is linked to (B) a structural nucleic acid molecule, wherein the structural nucleic acid molecule encodes a plant phosphogluconate pathway enzyme or fragment thereof, the structural nucleic acid molecule comprising a nucleic acid sequence selected from the group consisting of SEQ ID NO: 1 through SEQ ID NO: 699 or fragment

15   thereof; which is linked to (C) a 3' non-translated sequence that functions in the plant cell to cause termination of transcription and addition of polyadenylated ribonucleotides to a 3' end of the mRNA molecule.

The present invention also provides a transformed plant having a nucleic acid molecule which comprises: (A) an exogenous promoter region which functions in a plant cell to cause the

20   production of a mRNA molecule; which is linked to (B) a structural nucleic acid molecule, wherein the structural nucleic acid molecule is selected from the group consisting of a nucleic acid molecule that encodes for a glucose-6-phosphate-1-dehydrogenase enzyme or fragment thereof; a nucleic acid molecule that encodes for a 6-phosphogluconate dehydrogenase enzyme

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or fragment thereof; a nucleic acid molecule that encodes for a putative 6-phosphogluconate dehydrogenase enzyme or fragment thereof; a nucleic acid molecule that encodes for a D-ribulose-5-phosphate-3-epimerase enzyme or fragment thereof; a nucleic acid molecule that encodes for a ribose-5-phosphate isomerase enzyme or fragment thereof; a nucleic acid molecule

5   that encodes for a putative ribose-5-phosphate isomerase enzyme or fragment thereof; a nucleic acid molecule that encodes for a transketolase enzyme or fragment thereof; a nucleic acid molecule that encodes for a putative transketolase enzyme or fragment thereof; a nucleic acid molecule that encodes for a transaldolase enzyme or fragment thereof; a nucleic acid molecule that encodes for a putative transaldolase enzyme or fragment thereof; and a nucleic acid molecule

10   that encodes for a phosphoglucoisomerase enzyme or fragment thereof; which is linked to (C) a 3' non-translated sequence that functions in the plant cell to cause termination of transcription and addition of polyadenylated ribonucleotides to a 3' end of the mRNA molecule.

The present invention also provides a transformed plant having a nucleic acid molecule which comprises: (A) an exogenous promoter region which functions in a plant cell to cause the

15   production of a mRNA molecule; which is linked to (B) a transcribed nucleic acid molecule with a transcribed strand and a non-transcribed strand, wherein the transcribed strand is complementary to a nucleic acid molecule comprising a nucleic acid sequence selected from the group consisting of SEQ ID NO: 1 through SEQ ID NO: 699 or fragment thereof; which is linked to (C) a 3' non-translated sequence that functions in plant cells to cause termination of

20   transcription and addition of polyadenylated ribonucleotides to a 3' end of the mRNA molecule.

The present invention also provides a transformed plant having a nucleic acid molecule which comprises: (A) an exogenous promoter region which functions in a plant cell to cause the production of a mRNA molecule; which is linked to: (B) a transcribed nucleic acid molecule

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with a transcribed strand and a non-transcribed strand, wherein a transcribed mRNA of the transcribed strand is complementary to an endogenous mRNA molecule having a nucleic acid sequence selected from the group consisting of an endogenous mRNA molecule that encodes a maize or soybean glucose-6-phosphate-1-dehydrogenase enzyme or fragment thereof; an

5   endogenous mRNA molecule that encodes a maize or soybean 6-phosphogluconate dehydrogenase enzyme or fragment thereof; an endogenous mRNA molecule that encodes a putative maize or soybean 6-phosphogluconate dehydrogenase enzyme or fragment thereof; an endogenous mRNA molecule that encodes a maize or soybean D-ribulose-5-phosphate-3-epimerase enzyme or fragment thereof; an endogenous mRNA molecule that encodes a maize or

10   soybean ribose-5-phosphate isomerase enzyme or fragment thereof; an endogenous mRNA molecule that encodes a putative maize or soybean ribose-5-phosphate isomerase enzyme or fragment thereof; an endogenous mRNA molecule that encodes a maize or soybean transketolase enzyme or fragment thereof; an endogenous mRNA molecule that encodes a putative maize or soybean transketolase enzyme or fragment thereof; an endogenous mRNA molecule that encodes

15   a maize or soybean transaldolase enzyme or fragment thereof; an endogenous mRNA molecule that encodes a putative maize transaldolase enzyme or fragment thereof; and an endogenous mRNA molecule that encodes a maize or soybean phosphoglucoisomerase enzyme or fragment thereof; which is linked to (C) a 3' non-translated sequence that functions in the plant cell to cause termination of transcription and addition of polyadenylated ribonucleotides to a 3' end of

20   the mRNA molecule.

The present invention also provides a method for determining a level or pattern of a plant phosphogluconate pathway enzyme in a plant cell or plant tissue comprising: (A) incubating, under conditions permitting nucleic acid hybridization, a marker nucleic acid molecule, the

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marker nucleic acid molecule having a nucleic acid sequence selected from the group consisting

of SEQ ID NO: 1 through SEQ ID NO: 699 or complements thereof or fragment of either, with a

complementary nucleic acid molecule obtained from the plant cell or plant tissue, wherein

nucleic acid hybridization between the marker nucleic acid molecule and the complementary

5   nucleic acid molecule obtained from the plant cell or plant tissue permits the detection of the

plant phosphogluconate pathway enzyme; (B) permitting hybridization between the marker

nucleic acid molecule and the complementary nucleic acid molecule obtained from the plant cell

or plant tissue; and (C) detecting the level or pattern of the complementary nucleic acid, wherein

the detection of the complementary nucleic acid is predictive of the level or pattern of the plant

10   phosphogluconate pathway enzyme.

The present invention also provides a method for determining a level or pattern of a plant

phosphogluconate pathway enzyme in a plant cell or plant tissue comprising: (A) incubating,

under conditions permitting nucleic acid hybridization, a marker nucleic acid molecule, the

marker nucleic acid molecule comprising a nucleic acid molecule that encodes a maize or

15   soybean glucose-6-phosphate-1-dehydrogenase enzyme or complement thereof or fragment of

either; a nucleic acid molecule that encodes a maize or soybean 6-phosphogluconate

dehydrogenase enzyme or complement thereof or fragment of either; a nucleic acid molecule that

encodes a maize or soybean putative 6-phosphogluconate dehydrogenase enzyme or complement

thereof or fragment of either; a nucleic acid molecule that encodes a maize or soybean D-

20   ribulose-5-phosphate-3-epimerase enzyme or complement thereof or fragment of either; a nucleic

acid molecule that encodes a maize or soybean ribose-5-phosphate isomerase enzyme or

complement thereof or fragment of either; a nucleic acid molecule that encodes a putative maize

or soybean ribose-5-phosphate isomerase enzyme or complement thereof or fragment of either; a

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nucleic acid molecule that encodes a maize or soybean transketolase enzyme or complement thereof or fragment of either; a nucleic acid molecule that encodes a putative maize or soybean transketolase enzyme or complement thereof or fragment of either; a nucleic acid molecule that encodes a maize or soybean transaldolase enzyme or complement thereof or fragment of either; a

5   nucleic acid molecule that encodes a putative maize transaldolase enzyme or complement thereof or fragment of either; and a nucleic acid molecule that encodes a maize or soybean phosphoglucoisomerase enzyme or complement thereof or fragment of either; with a complementary nucleic acid molecule obtained from the plant cell or plant tissue, wherein nucleic acid hybridization between the marker nucleic acid molecule and the complementary

10   nucleic acid molecule obtained from the plant cell or plant tissue permits the detection of the plant phosphogluconate pathway enzyme; (B) permitting hybridization between the marker nucleic acid molecule and the complementary nucleic acid molecule obtained from the plant cell or plant tissue; and (C) detecting the level or pattern of the complementary nucleic acid, wherein the detection of the complementary nucleic acid is predictive of the level or pattern of the plant

15   phosphogluconate pathway enzyme.

The present invention also provides a method for determining a level or pattern of a plant phosphogluconate pathway enzyme in a plant cell or plant tissue under evaluation which comprises assaying the concentration of a molecule, whose concentration is dependent upon the expression of a gene, the gene specifically hybridizes to a nucleic acid molecule having a nucleic

20   acid sequence selected from the group consisting of SEQ ID NO: 1 through SEQ ID NO: 699 or complements thereof, in comparison to the concentration of that molecule present in a reference plant cell or a reference plant tissue with a known level or pattern of the plant phosphogluconate pathway enzyme, wherein the assayed concentration of the molecule is compared to the assayed

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concentration of the molecule in the reference plant cell or reference plant tissue with the known

level or pattern of the plant phosphogluconate pathway enzyme.

The present invention also provides a method for determining a level or pattern of a plant

phosphogluconate pathway enzyme in a plant cell or plant tissue under evaluation which

comprises assaying the concentration of a molecule, whose concentration is dependent upon the

expression of a gene, the gene specifically hybridizes to a nucleic acid molecule selected from

the group consisting of a nucleic acid molecule that encodes a maize or soybean glucose-6-

phosphate-1-dehydrogenase enzyme; a nucleic acid molecule that encodes a maize or soybean 6-

phosphogluconate dehydrogenase enzyme or complement thereof; a nucleic acid molecule that

encodes a putative maize or soybean 6-phosphogluconate dehydrogenase enzyme or complement

thereof; a nucleic acid molecule that encodes a maize or soybean D-ribulose-5-phosphate-3-

epimerase enzyme or complement thereof; a nucleic acid molecule that encodes a maize or

soybean ribose-5-phosphate isomerase enzyme or complement thereof; a nucleic acid molecule

that encodes a putative maize or soybean ribose-5-phosphate isomerase enzyme or complement

thereof; a nucleic acid molecule that encodes a maize or soybean transketolase enzyme or

complement thereof; a nucleic acid molecule that encodes a putative maize or soybean

transketolase enzyme or complement thereof; a nucleic acid molecule that encodes a maize or

soybean transaldolase enzyme or complement thereof; a nucleic acid molecule that encodes a

putative maize transaldolase enzyme or complement thereof; and a nucleic acid molecule that

encodes a maize or soybean phosphoglucoisomerase enzyme or complement thereof; in

comparison to the concentration of that molecule present in a reference plant cell or a reference

plant tissue with a known level or pattern of the plant phosphogluconate pathway enzyme,

wherein the assayed concentration of the molecule is compared to the assayed concentration of

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the molecule in the reference plant cell or the reference plant tissue with the known level or pattern of the plant phosphogluconate pathway enzyme.

The present invention provides a method of determining a mutation in a plant whose presence is predictive of a mutation affecting a level or pattern of a protein comprising the steps:

5   (A) incubating, under conditions permitting nucleic acid hybridization, a marker nucleic acid, the marker nucleic acid selected from the group of marker nucleic acid molecules which specifically hybridize to a nucleic acid molecule having a nucleic acid sequence selected from the group of SEQ ID NO: 1 through SEQ ID NO: 699 or complements thereof or fragment of either and a complementary nucleic acid molecule obtained from the plant, wherein nucleic acid

10   hybridization between the marker nucleic acid molecule and the complementary nucleic acid molecule obtained from the plant permits the detection of a polymorphism whose presence is predictive of a mutation affecting the level or pattern of the protein in the plant; (B) permitting hybridization between the marker nucleic acid molecule and the complementary nucleic acid molecule obtained from the plant; and (C) detecting the presence of the polymorphism, wherein

15   the detection of the polymorphism is predictive of the mutation.

The present invention also provides a method for determining a mutation in a plant whose presence is predictive of a mutation affecting the level or pattern of a plant phosphogluconate pathway enzyme comprising the steps: (A) incubating, under conditions permitting nucleic acid hybridization, a marker nucleic acid molecule, the marker nucleic acid molecule comprising a

20   nucleic acid molecule that is linked to a gene, the gene specifically hybridizes to a nucleic acid molecule having a nucleic acid sequence selected from the group consisting of SEQ ID NO: 1 through SEQ ID NO: 699 or complements thereof and a complementary nucleic acid molecule obtained from the plant, wherein nucleic acid hybridization between the marker nucleic acid

molecule and the complementary nucleic acid molecule obtained from the plant permits the

detection of a polymorphism whose presence is predictive of a mutation affecting the level or

pattern of the plant phosphogluconate pathway enzyme in the plant; (B) permitting hybridization

between the marker nucleic acid molecule and the complementary nucleic acid molecule

5   obtained from the plant; and (C) detecting the presence of the polymorphism, wherein the

detection of the polymorphism is predictive of the mutation.

The present invention also provides a method for determining a mutation in a plant whose

presence is predictive of a mutation affecting the level or pattern of a plant phosphogluconate

pathway enzyme comprising the steps: (A) incubating, under conditions permitting nucleic acid

10   hybridization, a marker nucleic acid molecule, the marker nucleic acid molecule comprising a

nucleic acid molecule that is linked to a gene, the gene specifically hybridizes to a nucleic acid

molecule selected from the group consisting of a nucleic acid molecule that encodes a maize or

soybean glucose-6-phosphate-1-dehydrogenase enzyme or complement thereof; a nucleic acid

molecule that encodes a maize or soybean 6-phosphogluconate dehydrogenase enzyme or

15   complement thereof; a nucleic acid molecule that encodes a putative maize or soybean 6-

phosphogluconate dehydrogenase enzyme or complement thereof; a nucleic acid molecule that

encodes a maize or soybean D-ribulose-5-phosphate-3-epimerase enzyme or complement

thereof; a nucleic acid molecule that encodes a maize or soybean ribose-5-phosphate isomerase

enzyme or complement thereof; a nucleic acid molecule that encodes a putative maize or soybean

20   ribose-5-phosphate isomerase enzyme or complement thereof; a nucleic acid molecule that

encodes a maize or soybean transketolase enzyme or complement thereof; a nucleic acid

molecule that encodes a putative maize or soybean transketolase enzyme or complement thereof;

a nucleic acid molecule that encodes a maize or soybean transaldolase enzyme or complement

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thereof; a nucleic acid molecule that encodes a putative maize or soybean transaldolase enzyme or complement thereof; a nucleic acid molecule that encodes a maize or soybean phosphoglucoisomerase enzyme or complement thereof; and a complementary nucleic acid molecule obtained from the plant, wherein nucleic acid hybridization between the marker nucleic

5   acid molecule and the complementary nucleic acid molecule obtained from the plant permits the detection of a polymorphism whose presence is predictive of a mutation affecting the level or pattern of the plant phosphogluconate pathway enzyme in the plant; (B) permitting hybridization between the marker nucleic acid molecule and the complementary nucleic acid molecule obtained from the plant; and (C) detecting the presence of the polymorphism, wherein the

10   detection of the polymorphism is predictive of the mutation.

The present invention also provides a method of producing a plant containing an overexpressed protein comprising: (A) transforming the plant with a functional nucleic acid molecule, wherein the functional nucleic acid molecule comprises a promoter region, wherein the promoter region is linked to a structural region, wherein the structural region has a nucleic acid

15   sequence selected from group consisting of SEQ ID NO: 1 through SEQ ID NO: 699; wherein the structural region is linked to a 3' non-translated sequence that functions in the plant to cause termination of transcription and addition of polyadenylated ribonucleotides to a 3' end of a mRNA molecule; and wherein the functional nucleic acid molecule results in overexpression of the protein; and (B) growing the transformed plant.

20   The present invention also provides a method of producing a plant containing an overexpressed plant phosphogluconate pathway enzyme comprising: (A) transforming the plant with a functional nucleic acid molecule, wherein the functional nucleic acid molecule comprises a promoter region, wherein the promoter region is linked to a structural region, wherein the

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structural region comprises a nucleic acid molecule having a nucleic acid sequence selected from

the group consisting of SEQ ID NO: 1 through SEQ ID NO: 699 or fragment thereof; wherein

the structural region is linked to a 3' non-translated sequence that functions in the plant to cause

termination of transcription and addition of polyadenylated ribonucleotides to a 3' end of a

5   mRNA molecule; and wherein the functional nucleic acid molecule results in overexpression of

the plant phosphogluconate pathway enzyme; and (B) growing the transformed plant.

The present invention also provides a method of producing a plant containing an

overexpressed plant phosphogluconate pathway enzyme comprising: (A) transforming the plant

with a functional nucleic acid molecule, wherein the functional nucleic acid molecule comprises

10   a promoter region, wherein the promoter region is linked to a structural region, wherein the

structural region comprises a nucleic acid molecule selected from the group consisting of a

nucleic acid molecule that encodes a maize or soybean glucose-6-phosphate-1-dehydrogenase

enzyme or fragment thereof; a nucleic acid molecule that encodes a maize or soybean 6-

phosphogluconate dehydrogenase enzyme or fragment thereof; a nucleic acid molecule that

15   encodes a putative maize or soybean 6-phosphogluconate dehydrogenase enzyme or fragment

thereof; a nucleic acid molecule that encodes a maize or soybean D-ribulose-5-phosphate-3-

epimerase enzyme or fragment thereof; a nucleic acid molecule that encodes a maize or soybean

ribose-5-phosphate isomerase enzyme or fragment thereof; a nucleic acid molecule that encodes

a putative maize or soybean ribose-5-phosphate isomerase enzyme or fragment thereof; a nucleic

20   acid molecule that encodes a maize or soybean transketolase enzyme or fragment thereof; a

nucleic acid molecule that encodes a putative maize or soybean transketolase enzyme or

fragment thereof; a nucleic acid molecule that encodes a maize or soybean transaldolase enzyme

or fragment thereof; a nucleic acid molecule that encodes a putative maize transaldolase enzyme

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or fragment thereof; a nucleic acid molecule that encodes a maize or soybean

phosphoglucoisomerase enzyme or fragment thereof; wherein the structural region is linked to a

3' non-translated sequence that functions in the plant to cause termination of transcription and

addition of polyadenylated ribonucleotides to a 3' end of a mRNA molecule; and wherein the

5   functional nucleic acid molecule results in overexpression of the plant phosphogluconate

pathway enzyme; and (B) growing the transformed plant.

The present invention also provides a method of producing a plant containing reduced

levels of a plant phosphogluconate pathway enzyme comprising: (A) transforming the plant with

a functional nucleic acid molecule, wherein the functional nucleic acid molecule comprises a

10   promoter region, wherein the promoter region is linked to a structural region, wherein the

structural region comprises a nucleic acid molecule having a nucleic acid sequence selected from

the group consisting of SEQ ID NO: 1 through SEQ ID NO: 699; wherein the structural region is

linked to a 3' non-translated sequence that functions in the plant to cause termination of

transcription and addition of polyadenylated ribonucleotides to a 3' end of a mRNA molecule;

15   and wherein the functional nucleic acid molecule results in co-suppression of the plant

phosphogluconate pathway enzyme; and (B) growing the transformed plant.

The present invention also provides a method of producing a plant containing reduced

levels of a plant phosphogluconate pathway enzyme comprising: (A) transforming the plant with

a functional nucleic acid molecule, wherein the functional nucleic acid molecule comprises a

20   promoter region, wherein the promoter region is linked to a structural region, wherein the

structural region comprises a nucleic acid molecule having a nucleic acid sequence selected from

the group consisting of a nucleic acid molecule that encodes a maize or soybean glucose-6-

phosphate-1-dehydrogenase enzyme or fragment thereof; a nucleic acid molecule that encodes a

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maize or soybean 6-phosphogluconate dehydrogenase enzyme or fragment thereof; a nucleic acid molecule that encodes a maize or soybean putative 6-phosphogluconate dehydrogenase enzyme or fragment thereof; a nucleic acid molecule that encodes a maize or soybean D-ribulose-5-phosphate-3-epimerase enzyme or fragment thereof; a nucleic acid molecule that encodes a

5   maize or soybean ribose-5-phosphate isomerase enzyme or fragment thereof; a nucleic acid molecule that encodes a putative maize or soybean ribose-5-phosphate isomerase enzyme or fragment thereof; a nucleic acid molecule that encodes a maize or soybean transketolase enzyme or fragment thereof; a nucleic acid molecule that encodes a putative maize or soybean transketolase enzyme or fragment thereof; a nucleic acid molecule that encodes a maize or

10   soybean transaldolase enzyme or fragment thereof; a nucleic acid molecule that encodes a putative maize transaldolase enzyme or fragment thereof; a nucleic acid molecule that encodes a maize or soybean phosphoglucoisomerase enzyme or fragment thereof; wherein the structural region is linked to a 3' non-translated sequence that functions in the plant to cause termination of transcription and addition of polyadenylated ribonucleotides to a 3' end of a mRNA molecule;

15   and wherein the functional nucleic acid molecule results in co-suppression of the plant phosphogluconate pathway enzyme; and (B) growing the transformed plant.

The present invention also provides a method for reducing expression of a plant phosphogluconate pathway enzyme in a plant comprising: (A) transforming the plant with a nucleic acid molecule, the nucleic acid molecule having an exogenous promoter region which

20   functions in a plant cell to cause the production of a mRNA molecule, wherein the exogenous promoter region is linked to a transcribed nucleic acid molecule having a transcribed strand and a non-transcribed strand, wherein the transcribed strand is complementary to a nucleic acid molecule having a nucleic acid sequence selected from the group consisting of SEQ ID NO: 1

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through SEQ ID NO: 699 or complements thereof or fragments of either and the transcribed

strand is complementary to an endogenous mRNA molecule; and wherein the transcribed nucleic

acid molecule is linked to a 3' non-translated sequence that functions in the plant cell to cause

termination of transcription and addition of polyadenylated ribonucleotides to a 3' end of a

5   mRNA molecule; and (B) growing the transformed plant.

The present invention also provides a method for reducing expression of a plant

phosphogluconate pathway enzyme in a plant comprising: (A) transforming the plant with a

nucleic acid molecule, the nucleic acid molecule having an exogenous promoter region which

functions in a plant cell to cause the production of a mRNA molecule, wherein the exogenous

10   promoter region is linked to a transcribed nucleic acid molecule having a transcribed strand and a

non-transcribed strand, wherein a transcribed mRNA of the transcribed strand is complementary

to a nucleic acid molecule selected from the group consisting of an endogenous mRNA molecule

that encodes a maize or soybean glucose-6-phosphate-1-dehydrogenase enzyme or fragment

thereof; an endogenous mRNA molecule that encodes a maize or soybean 6-phosphogluconate

15   dehydrogenase enzyme or fragment thereof; an endogenous mRNA molecule that encodes a

putative maize or soybean 6-phosphogluconate dehydrogenase enzyme or fragment thereof; an

endogenous mRNA molecule that encodes a maize or soybean D-ribulose-5-phosphate-3-

epimerase enzyme or fragment thereof; an endogenous mRNA molecule that encodes a maize or

soybean ribose-5-phosphate isomerase enzyme or fragment thereof; an endogenous mRNA

20   molecule that encodes a putative maize or soybean ribose-5-phosphate isomerase enzyme or

fragment thereof; an endogenous mRNA molecule that encodes a maize or soybean transketolase

enzyme or fragment thereof; an endogenous mRNA molecule that encodes a putative maize or

soybean transketolase enzyme or fragment thereof; an endogenous mRNA molecule that encodes

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a maize or soybean transaldolase enzyme or fragment thereof; an endogenous mRNA molecule that encodes a putative maize transaldolase enzyme or fragment thereof; an endogenous mRNA molecule that encodes a maize or soybean phosphoglucoisomerase enzyme or fragment thereof; and wherein the transcribed nucleic acid molecule is linked to a 3' non-translated sequence that

5 functions in the plant cell to cause termination of transcription and addition of polyadenylated ribonucleotides to a 3' end of a mRNA molecule; and (B) growing the transformed plant.

The present invention also provides a method of determining an association between a polymorphism and a plant trait comprising: (A) hybridizing a nucleic acid molecule specific for the polymorphism to genetic material of a plant, wherein the nucleic acid molecule has a nucleic

10 acid sequence selected from the group consisting of SEQ ID NO: 1 through SEQ ID NO: 699 or complements thereof or fragment of either; and (B) calculating the degree of association between the polymorphism and the plant trait.

The present invention also provides a method of determining an association between a polymorphism and a plant trait comprising: (A) hybridizing a nucleic acid molecule specific for

15 the polymorphism to genetic material of a plant, wherein the nucleic acid molecule is selected from the group consisting of a nucleic acid molecule that encodes a maize or soybean glucose-6-phosphate-1-dehydrogenase enzyme or complement thereof or fragment of either; a nucleic acid molecule that encodes a maize or soybean 6-phosphogluconate dehydrogenase enzyme or complement thereof or fragment of either; a nucleic acid molecule that encodes a putative maize

20 or soybean 6-phosphogluconate dehydrogenase enzyme or complement thereof or fragment of either; a nucleic acid molecule that encodes a maize or soybean D-ribulose-5-phosphate-3-epimerase enzyme or complement thereof or fragment of either; a nucleic acid molecule that encodes a maize or soybean ribose-5-phosphate isomerase enzyme or complement thereof or

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fragment of either; a nucleic acid molecule that encodes a putative maize or soybean ribose-5-phosphate isomerase enzyme or complement thereof or fragment of either; a nucleic acid molecule that encodes a maize or soybean transketolase enzyme or complement thereof or fragment of either; a nucleic acid molecule that encodes a putative maize or soybean

5   transketolase enzyme or complement thereof or fragment of either; a nucleic acid molecule that encodes a maize or soybean transaldolase enzyme or complement thereof or fragment of either; a nucleic acid molecule that encodes a putative maize transaldolase enzyme or complement thereof or fragment of either; and a nucleic acid molecule that encodes a maize or soybean phosphoglucoisomerase enzyme or complement thereof or fragment of either; and (B) calculating

10   the degree of association between the polymorphism and the plant trait.

The present invention also provides a method of isolating a nucleic acid that encodes a plant phosphogluconate pathway enzyme or fragment thereof comprising: (A) incubating under conditions permitting nucleic acid hybridization, a first nucleic acid molecule comprising a nucleic acid sequence selected from the group consisting of SEQ ID NO: 1 through SEQ ID NO:

15   699 or complements thereof or fragment of either with a complementary second nucleic acid molecule obtained from a plant cell or plant tissue; (B) permitting hybridization between the first nucleic acid molecule and the second nucleic acid molecule obtained from the plant cell or plant tissue; and (C) isolating the second nucleic acid molecule.

The present invention also provides a method of isolating a nucleic acid molecule that

20   encodes a plant phosphogluconate pathway enzyme or fragment thereof comprising: (A) incubating under conditions permitting nucleic acid hybridization, a first nucleic acid molecule selected from the group consisting of a nucleic acid molecule that encodes a maize or soybean glucose-6-phosphate-1-dehydrogenase enzyme or complement thereof or fragment of either; a

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nucleic acid molecule that encodes a maize or soybean 6-phosphogluconate dehydrogenase enzyme or complement thereof or fragment of either; a nucleic acid molecule that encodes a putative maize or soybean 6-phosphogluconate dehydrogenase enzyme or complement thereof or fragment of either; a nucleic acid molecule that encodes a maize or soybean D-ribulose-5-

5 phosphate-3-epimerase enzyme or complement thereof or fragment of either; a nucleic acid molecule that encodes a maize or soybean ribose-5-phosphate isomerase enzyme or complement thereof or fragment of either; a nucleic acid molecule that encodes a putative maize or soybean ribose-5-phosphate isomerase enzyme or complement thereof or fragment of either; a nucleic acid molecule that encodes a maize or soybean transketolase enzyme or complement thereof or

10 fragment of either; a nucleic acid molecule that encodes a putative maize or soybean transketolase enzyme or complement thereof or fragment of either; a nucleic acid molecule that encodes a maize or soybean transaldolase enzyme or complement thereof or fragment of either; a nucleic acid molecule that encodes a putative maize transaldolase enzyme or complement thereof or fragment of either; and a nucleic acid molecule that encodes a maize or soybean

15 phosphoglucoisomerase enzyme or complement thereof or fragment of either; with a complementary second nucleic acid molecule obtained from a plant cell or plant tissue; (B) permitting hybridization between the plant phosphogluconate pathway enzyme nucleic acid molecule and the complementary nucleic acid molecule obtained from the plant cell or plant tissue; and (C) isolating the second nucleic acid molecule.

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DETAILED DESCRIPTION OF THE INVENTION

Definitions and Agents of the Present Invention

Definitions:

As used herein, a phosphogluconate pathway enzyme is any enzyme that is associated with the synthesis, oxidation, hydrolysis, or modification of phosphogluconate compounds.

As used herein, a phosphogluconate synthesis enzyme is any enzyme that is associated with the synthesis of phosphogluconate.

As used herein, a phosphogluconate oxidation enzyme is any enzyme that is associated with the oxidation of phosphogluconate.

As used herein, a phosphogluconate hydrolysis enzyme is any enzyme that is associated with the hydrolysis of phosphogluconate.

As used herein, a phosphogluconate modification enzyme is any enzyme that is associated with the modification of phosphogluconate compounds.

As used herein, glucose-6-phosphate dehydrogenase is any enzyme that catalyzes the conversion of glucose-6-phosphate to 6-phosphoglyconolactone.

As used herein, 6-phosphogluconate dehydrogenase is any enzyme that catalyzes the conversion of 6-phosphogluconate to ribulose-5-phosphate.

As used herein, ribose-5-phosphate isomerase is any enzyme that catalyzes the conversion of ribulose-5-phosphate to ribose-5-phosphate.

As used herein, ribulose-5-phosphate-3-epimerase is any enzyme that catalyzes the conversion of ribulose-5-phosphate to xylulose-5-phosphate.

As used herein, transketolase is any enzyme that catalyzes the conversion of ribose-5-phosphate and xylulose-5-phosphate to sedheptulose-7-phosphate and 3-phosphoglyceraldehyde.

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As used herein, transaldolase is any enzyme that catalyzes the conversion of sedheptulose-7-phosphate and 3-phosphoglyceraldehyde to erythrose-4-phosphate and fructose-6-phosphate.

As used herein, phosphohexose isomerase (phsophoglucoisomerase) is any enzyme that catalyzes the conversion of fructose-6-phosphate to glucose-6-phosphate.

Agents

(a)   Nucleic Acid Molecules

Agents of the present invention include plant nucleic acid molecules and more preferably include maize and soybean nucleic acid molecules and more preferably include nucleic acid molecules of the maize genotypes B73 (Illinois Foundation Seeds, Champaign, Illinois U.S.A.), B73 x Mo17 (Illinois Foundation Seeds, Champaign, Illinois U.S.A.), DK604 (Dekalb Genetics, Dekalb, Illinois U.S.A.), H99 (Illinois Foundation Seeds, Champaign, Illinois U.S.A.), RX601 (Asgrow Seed Company, Des Moines, Iowa), Mo17 (Illinois Foundation Seeds, Champaign, Illinois U.S.A.), and soybean types Asgrow 3244 (Asgrow Seed Company, Des Moines, Iowa), C1944 (United States Department of Agriculture (USDA) Soybean Germplasm Collection, Urbana, Illinois U.S.A.), Cristalina (USDA Soybean Germplasm Collection, Urbana, Illinois U.S.A.), FT108 (Monsoy, Brazil), Hartwig (USDA Soybean Germplasm Collection, Urbana, Illinois U.S.A.), BW211S Null (Tohoku University, Morioka, Japan), PI507354 (USDA Soybean Germplasm Collection, Urbana, Illinois U.S.A.), Asgrow A4922 (Asgrow Seed Company, Des Moines, Iowa U.S.A.), PI227687 (USDA Soybean Germplasm Collection, Urbana, Illinois U.S.A.), PI229358 (USDA Soybean Germplasm Collection, Urbana, Illinois U.S.A.) and Asgrow A3237 (Asgrow Seed Company, Des Moines, Iowa U.S.A.).

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A subset of the nucleic acid molecules of the present invention includes nucleic acid molecules that are marker molecules. Another subset of the nucleic acid molecules of the present invention include nucleic acid molecules that encode a protein or fragment thereof. Another subset of the nucleic acid molecules of the present invention are EST molecules.

5   Fragment nucleic acid molecules may encode significant portion(s) of, or indeed most of, these nucleic acid molecules. Alternatively, the fragments may comprise smaller oligonucleotides (having from about 15 to about 250 nucleotide residues and more preferably, about 15 to about 30 nucleotide residues).

The term "substantially purified", as used herein, refers to a molecule separated from

10   substantially all other molecules normally associated with it in its native state. More preferably a substantially purified molecule is the predominant species present in a preparation. A substantially purified molecule may be greater than 60% free, preferably 75% free, more preferably 90% free, and most preferably 95% free from the other molecules (exclusive of solvent) present in the natural mixture. The term "substantially purified" is not intended to

15   encompass molecules present in their native state.

The agents of the present invention will preferably be "biologically active" with respect to either a structural attribute, such as the capacity of a nucleic acid to hybridize to another nucleic acid molecule, or the ability of a protein to be bound by an antibody (or to compete with another molecule for such binding). Alternatively, such an attribute may be catalytic and thus

20   involve the capacity of the agent to mediate a chemical reaction or response.

The agents of the present invention may also be recombinant. As used herein, the term recombinant means any agent (e.g. DNA, peptide etc.), that is, or results, however indirect, from human manipulation of a nucleic acid molecule.

It is understood that the agents of the present invention may be labeled with reagents that facilitate detection of the agent (e.g. fluorescent labels, Prober *et al., Science 238*:336-340 (1987); Albarella *et al.,* EP 144914; chemical labels, Sheldon *et al.,* U.S. Patent No. 4,582,789; Albarella *et al.,* U.S. Patent No. 4,563,417; modified bases, Miyoshi *et al.,* EP 119448, all of

5   which are hereby incorporated by reference in their entirety).

It is further understood, that the present invention provides recombinant bacterial, mammalian, microbial, insect, fungal and plant cells and viral constructs comprising the agents of the present invention. (See, for example, Uses of the Agents of the Invention, Section (a) Plant Constructs and Plant Transformants; Section (b) Fungal Constructs and Fungal

10   Transformants; Section (c) Mammalian Constructs and Transformed Mammalian Cells; Section (d) Insect Constructs and Transformed Insect Cells; and Section (e) Bacterial Constructs and Transformed Bacterial Cells)

Nucleic acid molecules or fragments thereof of the present invention are capable of specifically hybridizing to other nucleic acid molecules under certain circumstances. As used

15   herein, two nucleic acid molecules are said to be capable of specifically hybridizing to one another if the two molecules are capable of forming an anti-parallel, double-stranded nucleic acid structure. A nucleic acid molecule is said to be the "complement" of another nucleic acid molecule if they exhibit complete complementarity. As used herein, molecules are said to exhibit "complete complementarity" when every nucleotide of one of the molecules is

20   complementary to a nucleotide of the other. Two molecules are said to be "minimally complementary" if they can hybridize to one another with sufficient stability to permit them to remain annealed to one another under at least conventional "low-stringency" conditions. Similarly, the molecules are said to be "complementary" if they can hybridize to one another

with sufficient stability to permit them to remain annealed to one another under conventional "high-stringency" conditions. Conventional stringency conditions are described by Sambrook *et al., Molecular Cloning,* A Laboratory Manual, 2nd Ed., Cold Spring Harbor Press, Cold Spring Harbor, New York (1989) and by Haymes *et al., Nucleic Acid Hybridization, A Practical*

5   *Approach,* IRL Press, Washington, DC (1985), the entirety of which is herein incorporated by reference. Departures from complete complementarity are therefore permissible, as long as such departures do not completely preclude the capacity of the molecules to form a double-stranded structure. Thus, in order for a nucleic acid molecule to serve as a primer or probe it need only be sufficiently complementary in sequence to be able to form a stable double-stranded structure

10   under the particular solvent and salt concentrations employed.

Appropriate stringency conditions which promote DNA hybridization, for example, 6.0 X sodium chloride/sodium citrate (SSC) at about 45°C, followed by a wash of 2.0 X SSC at 50°C, are known to those skilled in the art or can be found in *Current Protocols in Molecular Biology,* John Wiley & Sons, N.Y. (1989), 6.3.1-6.3.6. For example, the salt concentration in the wash

15   step can be selected from a low stringency of about 2.0 X SSC at 50°C to a high stringency of about 0.2 X SSC at 50°C. In addition, the temperature in the wash step can be increased from low stringency conditions at room temperature, about 22°C, to high stringency conditions at about 65°C. Both temperature and salt may be varied, or either the temperature or the salt concentration may be held constant while the other variable is changed.

20   In a preferred embodiment, a nucleic acid of the present invention will specifically hybridize to one or more of the nucleic acid molecules set forth in SEQ ID NO: 1 through SEQ ID NO: 699 or complements thereof under moderately stringent conditions, for example at about 2.0 X SSC and about 65°C.

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In a particularly preferred embodiment, a nucleic acid of the present invention will include those nucleic acid molecules that specifically hybridize to one or more of the nucleic acid molecules set forth in SEQ ID NO: 1 through SEQ ID NO: 699 or complements thereof under high stringency conditions such as 0.2 X SSC and about 65°C.

5   In one aspect of the present invention, the nucleic acid molecules of the present invention have one or more of the nucleic acid sequences set forth in SEQ ID NO: 1 through SEQ ID NO: 699 or complements thereof. In another aspect of the present invention, one or more of the nucleic acid molecules of the present invention share between 100% and 90% sequence identity with one or more of the nucleic acid sequences set forth in SEQ ID NO: 1 through SEQ ID NO: 699 or complements thereof. In a further aspect of the present invention, one or more of the nucleic acid molecules of the present invention share between 100% and 95% sequence identity with one or more of the nucleic acid sequences set forth in SEQ ID NO: 1 through SEQ ID NO: 699 or complements thereof. In a more preferred aspect of the present invention, one or more of the nucleic acid molecules of the present invention share between 100% and 98% sequence identity with one or more of the nucleic acid sequences set forth in SEQ ID NO: 1 through SEQ ID NO: 699 or complements thereof. In an even more preferred aspect of the present invention, one or more of the nucleic acid molecules of the present invention share between 100% and 99% sequence identity with one or more of the sequences set forth in SEQ ID NO: 1 through SEQ ID NO: 699 or complements thereof.

20   In a further more preferred aspect of the present invention, one or more of the nucleic acid molecules of the present invention exhibit 100% sequence identity with a nucleic acid molecule present within MONN01, SATMON001, SATMON003 through SATMON014, SATMON016, SATMON017, SATMON019 through SATMON031, SATMON033,

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SATMON034, SATMONN01, SATMONN04 through SATMONN06, LIB36, LIB83 through LIB84, CMz029 through CMz031, CMz033 through CMz037, CMz039 through CMz042, CMz044 through CMz045, CMz047 through CMz050, SOYMON001 through SOYMON038, Soy51 through Soy56, Soy58 through Soy62, Soy65 through Soy77, LIB3054, LIB3087, and

5   LIB3094 (Monsanto Company, St. Louis, Missouri U.S.A.).

(i)   Nucleic Acid Molecules Encoding Proteins or Fragments Thereof

Nucleic acid molecules of the present invention can comprise sequences that encode a phosphogluconate pathway enzyme or fragment thereof. Such phosphogluconate pathway enzymes or fragments thereof include homologues of known phosphogluconate pathway

10   enzymes in other organisms.

In a preferred embodiment of the present invention, a maize or soybean phosphogluconate pathway enzyme or fragment thereof of the present invention is a homologue of another plant phosphogluconate pathway enzyme. In another preferred embodiment of the present invention, a maize or soybean phosphogluconate pathway enzyme or fragment thereof of

15   the present invention is a homologue of a fungal phosphogluconate pathway enzyme. In another preferred embodiment of the present invention, a maize or soybean phosphogluconate pathway enzyme or fragment thereof of the present invention is a homologue of a bacterial phosphogluconate pathway enzyme. In another preferred embodiment of the present invention, a soybean phosphogluconate pathway enzyme or fragment thereof of the present invention is a

20   homologue of a maize phosphogluconate pathway enzyme. In another preferred embodiment of the present invention, a maize phosphogluconate pathway enzyme homologue or fragment thereof of the present invention is a homologue of a soybean phosphogluconate pathway enzyme. In another preferred embodiment of the present invention, a maize or soybean phosphogluconate

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pathway enzyme homologue or fragment thereof of the present invention is a homologue of an

Arabidopsis thaliana phosphogluconate pathway enzyme.

In a preferred embodiment of the present invention, the nucleic molecule of the present

invention encodes a maize or soybean phosphogluconate pathway enzyme or fragment thereof

where a maize or soybean phosphogluconate pathway enzyme exhibits a BLAST probability

score of greater than 1E-12, preferably a BLAST probability score of between about 1E-30 and

about 1E-12, even more preferably a BLAST probability score of greater than 1E-30 with its

homologue.

In another preferred embodiment of the present invention, the nucleic acid molecule

encoding a maize or soybean phosphogluconate pathway enzyme or fragment thereof exhibits a

% identity with its homologue of between about 25% and about 40%, more preferably of

between about 40 and about 70%, even more preferably of between about 70% and about 90%

and even more preferably between about 90% and 99%. In another preferred embodiment of the

present invention, a maize or soybean phosphogluconate pathway enzyme or fragments thereof

exhibits a % identity with its homologue of 100%.

In a preferred embodiment of the present invention, the nucleic molecule of the present

invention encodes a maize or soybean phosphogluconate pathway enzyme or fragment thereof

where a maize or soybean phosphogluconate pathway enzyme exhibits a BLAST score of greater

than 120, preferably a BLAST score of between about 1450 and about 120, even more preferably

a BLAST score of greater than 1450 with its homologue.

Nucleic acid molecules of the present invention also include non-maize, non-soybean

homologues. Preferred non-maize, non-soybean homologues are selected from the group

consisting of alfalfa, *Arabidopsis,* barley, *Brassica*, broccoli, cabbage, citrus, cotton, garlic, oat,

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oilseed rape, onion, canola, flax, an ornamental plant, pea, peanut, pepper, potato, rice, rye,

sorghum, strawberry, sugarcane, sugarbeet, tomato, wheat, poplar, pine, fir, eucalyptus, apple,

lettuce, lentils, grape, banana, tea, turf grasses, sunflower, oil palm and *Phaseolus*.

In a preferred embodiment, nucleic acid molecules having SEQ ID NO: 1 through SEQ

5   ID NO: 699 or complements and fragments of either can be utilized to obtain such homologues.

The degeneracy of the genetic code, which allows different nucleic acid sequences to

code for the same protein or peptide, is known in the literature. (U.S. Patent No. 4,757,006, the

entirety of which is herein incorporated by reference).

In an aspect of the present invention, one or more of the nucleic acid molecules of the

10   present invention differ in nucleic acid sequence from those encoding a maize or soybean

phosphogluconate pathway enzyme or fragment thereof in SEQ ID NO: 1 through SEQ ID NO:

699 due to the degeneracy in the genetic code in that they encode the same phosphogluconate

pathway enzyme but differ in nucleic acid sequence.

In another further aspect of the present invention, one or more of the nucleic acid

15   molecules of the present invention differ in nucleic acid sequence from those encoding a maize

or soybean phosphogluconate pathway enzyme or fragment thereof in SEQ ID NO: 1 through

SEQ ID NO: 699 due to fact that the different nucleic acid sequence encodes a phosphogluconate

pathway enzyme having one or more conservative amino acid residue. Examples of conservative

substitutions are set forth in Table 1. It is understood that codons capable of coding for such

20   conservative substitutions are known in the art.

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Table 1

Original Residue	Conservative Substitutions
Ala	Ser
Arg	Lys
Asn	Gln; His
Asp	Glu
Cys	Ser; Ala
Gln	Asn
Glu	Asp
Gly	Pro
His	Asn; Gln
Ile	Leu; Val
Leu	Ile; Val
Lys	Arg; Gln; Glu
Met	Leu; Ile
Phe	Met; Leu; Tyr
Ser	Thr
Thr	Ser
Trp	Tyr
Tyr	Trp; Phe
Val	Ile; Leu

In a further aspect of the present invention, one or more of the nucleic acid molecules of the present invention differ in nucleic acid sequence from those encoding a maize or soybean phosphogluconate pathway enzyme or fragment thereof set forth in SEQ ID NO: 1 through SEQ ID NO: 699 or fragment thereof due to the fact that one or more codons encoding an amino acid has been substituted for a codon that encodes a nonessential substitution of the amino acid originally encoded.

Agents of the present invention include nucleic acid molecules that encode a maize or soybean phosphogluconate pathway enzyme or fragment thereof and particularly substantially purified nucleic acid molecules selected from the group consisting of a nucleic acid molecule that encodes a maize or soybean glucose-6-phosphate-1-dehydrogenase enzyme or fragment thereof; a nucleic acid molecule that encodes a maize or soybean 6-phosphogluconate dehydrogenase enzyme or fragment thereof; a nucleic acid molecule that encodes a putative maize or soybean 6-phosphogluconate dehydrogenase enzyme or fragment thereof; a nucleic acid molecule that encodes a maize or soybean D-ribulose-5-phosphate-3-epimerase enzyme or fragment thereof; a nucleic acid molecule that encodes a maize or soybean ribose-5-phosphate isomerase enzyme or fragment thereof; a nucleic acid molecule that encodes a putative maize or soybean ribose-5-phosphate isomerase enzyme or fragment thereof; a nucleic acid molecule that encodes a maize or soybean transketolase enzyme or fragment thereof; a nucleic acid molecule that encodes a putative maize or soybean transketolase enzyme or fragment thereof; a nucleic acid molecule that encodes a maize or soybean transkealdolase enzyme or fragment thereof a nucleic acid molecule that encodes a putative maize transaldolase enzyme or fragment thereof; a nucleic acid molecule that encodes a maize or soybean phosphoglucoisomerase enzyme or fragment thereof.

Non-limiting examples of such nucleic acid molecules of the present invention are

nucleic acid molecules comprising: SEQ ID NO: 1 through SEQ ID NO: 699 or fragment thereof

that encode for a plant phosphogluconate pathway enzyme or fragment thereof, SEQ ID NO: 1

through SEQ ID NO: 3 and SEQ ID NO: 4 through SEQ ID NO: 11 or fragment thereof that

5   encodes for a maize or soybean glucose-6-phosphate-1-dehydrogenase enzyme or fragment

thereof; SEQ ID NO: 12 through SEQ ID NO: 21 and SEQ ID NO: 22 through SEQ ID NO: 103

or fragment thereof that encodes for a maize or soybean 6-phosphogluconate dehydrogenase

enzyme or fragment thereof; SEQ ID NO: 104 through SEQ ID NO: 209 and SEQ ID NO: 210

through SEQ ID NO: 214 or fragment thereof that encodes for a putative maize or soybean 6-

10   phosphogluconate dehydrogenase enzyme or fragment thereof; SEQ ID NO: 215 through SEQ

ID NO: 260 and SEQ ID NO: 261 through SEQ ID NO: 299 or fragment thereof that encodes for

a maize or soybean D-ribulose-5-phosphate-3-epimerase enzyme or fragment thereof; SEQ ID

NO: 300 through SEQ ID NO: 306 and SEQ ID NO: 307 through SEQ ID NO: 311 or fragment

thereof that encodes for a maize or soybean ribose-5-phosphate isomerase enzyme or fragment

15   thereof; SEQ ID NO: 312 through SEQ ID NO: 313 and SEQ ID NO: 314 through SEQ ID NO:

318 or fragment thereof that encodes for a putative maize or soybean ribose-5-phosphate

isomerase enzyme or fragment thereof; SEQ ID NO: 319 through SEQ ID NO: 356 and SEQ ID

NO: 357 through SEQ ID NO: 437 or fragment thereof that encodes for a maize or soybean

transketolase enzyme or fragment thereof; SEQ ID NO: 438 through SEQ ID NO: 447 and SEQ

20   ID NO: 448 through SEQ ID NO: 453 or fragment thereof that encodes for a putative maize or

soybean transketolase enzyme or fragment thereof; SEQ ID NO: 454 through SEQ ID NO: 533

and SEQ ID NO: 534 through SEQ ID NO: 617 or fragment thereof that encodes for a maize or

soybean transaldolase enzyme or fragment thereof; SEQ ID NO: 618 or fragment thereof that

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encodes for a putative maize transaldolase enzyme or fragment thereof; and SEQ ID NO: 619 through SEQ ID NO: 683 and SEQ ID NO: 684 through SEQ ID NO: 699 or fragment thereof that encodes for a maize or soybean phosphoglucoisomerase enzyme or fragment thereof.

A nucleic acid molecule of the present invention can also encode an homologue of a maize or soybean glucose-6-phosphate-1-dehydrogenase enzyme or fragment thereof; a maize or soybean 6-phosphogluconate dehydrogenase enzyme or fragment thereof; a putative maize or soybean 6-phosphogluconate dehydrogenase enzyme or fragment thereof; a maize or soybean D-ribulose-5-phosphate-3-epimerase enzyme or fragment thereof; a maize or soybean ribose-5-phosphate isomerase enzyme or fragment thereof; a putative maize or soybean ribose-5-phosphate isomerase enzyme or fragment thereof; a maize or soybean transketolase enzyme or fragment thereof; a putative maize or soybean transketolase enzyme or fragment thereof; a maize or soybean transaldolase enzyme or fragment thereof; a putative maize transaldolase enzyme or fragment thereof; and a maize or soybean phosphoglucoisomerase enzyme or fragment thereof. As used herein a homologue protein molecule or fragment thereof is a counterpart protein molecule or fragment thereof in a second species (*e.g.*, maize copalyl diphosphate synthase is a homologue of *Arabidopsis* copalyl diphosphate synthase).

(ii)   Nucleic Acid Molecule Markers and Probes

One aspect of the present invention concerns markers that include nucleic acid molecules SEQ ID NO: 1 through SEQ ID NO: 699 or complements thereof or fragments of either that can act as markers or other nucleic acid molecules of the present invention that can act as markers. Genetic markers of the present invention include "dominant" or "codominant" markers "Codominant markers" reveal the presence of two or more alleles (two per diploid individual) at a locus. "Dominant markers" reveal the presence of only a single allele per locus. The presence

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of the dominant marker phenotype (e.g., a band of DNA) is an indication that one allele is present in either the homozygous or heterozygous condition. The absence of the dominant marker phenotype (e.g. absence of a DNA band) is merely evidence that "some other" undefined allele is present. In the case of populations where individuals are predominantly homozygous and loci are predominately dimorphic, dominant and codominant markers can be equally valuable. As populations become more heterozygous and multi-allelic, codominant markers often become more informative of the genotype than dominant markers. Marker molecules can be, for example, capable of detecting polymorphisms such as single nucleotide polymorphisms (SNPs).

SNPs are single base changes in genomic DNA sequence. They occur at greater frequency and are spaced with a greater uniformly throughout a genome than other reported forms of polymorphism. The greater frequency and uniformity of SNPs means that there is greater probability that such a polymorphism will be found near or in a genetic locus of interest than would be the case for other polymorphisms. SNPs are located in protein-coding regions and noncoding regions of a genome. Some of these SNPs may result in defective or variant protein expression (e.g., as a results of mutations or defective splicing). Analysis (genotyping) of characterized SNPs can require only a plus/minus assay rather than a lengthy measurement, permitting easier automation.

SNPs can be characterized using any of a variety of methods. Such methods include the direct or indirect sequencing of the site, the use of restriction enzymes (Botstein et al., Am. J. Hum. Genet. 32:314-331 (1980), the entirety of which is herein incorporated reference; Konieczny and Ausubel, Plant J. 4:403-410 (1993), the entirety of which is herein incorporated by reference), enzymatic and chemical mismatch assays (Myers et al., Nature 313:495-498

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(1985), the entirety of which is herein incorporated by reference), allele-specific PCR (Newton *et al.*, *Nucl. Acids Res.* *17*:2503-2516 (1989), the entirety of which is herein incorporated by reference; Wu *et al.*, *Proc. Natl. Acad. Sci. (U.S.A.)* *86*:2757-2760 (1989), the entirety of which is herein incorporated by reference), ligase chain reaction (Barany, *Proc. Natl. Acad. Sci.*

5   *(U.S.A.)* *88*:189-193 (1991), the entirety of which is herein incorporated by reference), single-strand conformation polymorphism analysis (Labrune *et al.*, *Am. J. Hum. Genet.* *48*: 1115-1120 (1991), the entirety of which is herein incorporated by reference), primer-directed nucleotide incorporation assays (Kuppuswami *et al.*, *Proc. Natl. Acad. Sci. USA* *88*:1143-1147 (1991), the entirety of which is herein incorporated by reference), dideoxy fingerprinting (Sarkar *et al.*,

10 *Genomics* *13*:441-443 (1992), the entirety of which is herein incorporated by reference), solid-phase ELISA-based oligonucleotide ligation assays (Nikiforov *et al.*, *Nucl. Acids Res.* *22*:4167-4175 (1994), the entirety of which is herein incorporated by reference), oligonucleotide fluorescence-quenching assays (Livak *et al.*, *PCR Methods Appl.* *4*:357-362 (1995), the entirety of which is herein incorporated by reference), 5'-nuclease allele-specific hybridization TaqMan

15 assay (Livak *et al.*, *Nature Genet.* *9*:341-342 (1995), the entirety of which is herein incorporated by reference), template-directed dye-terminator incorporation (TDI) assay (Chen and Kwok, *Nucl. Acids Res.* *25*:347-353 (1997), the entirety of which is herein incorporated by reference), allele-specific molecular beacon assay (Tyagi *et al.*, *Nature Biotech.* *16*: 49-53 (1998), the entirety of which is herein incorporated by reference), PinPoint assay (Haff and Smirnov,

20 *Genome Res.* *7*: 378-388 (1997), the entirety of which is herein incorporated by reference) and dCAPS analysis (Neff *et al.*, *Plant J.* *14*:387-392 (1998), the entirety of which is herein incorporated by reference).

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Additional markers, such as AFLP markers, RFLP markers and RAPD markers, can be utilized (Walton, *Seed World* 22-29 (July, 1993), the entirety of which is herein incorporated by reference; Burow and Blake, *Molecular Dissection of Complex Traits*, 13-29, Paterson (ed.), CRC Press, New York (1988), the entirety of which is herein incorporated by reference). DNA

5   markers can be developed from nucleic acid molecules using restriction endonucleases, the PCR and/or DNA sequence information. RFLP markers result from single base changes or insertions/deletions. These codominant markers are highly abundant in plant genomes, have a medium level of polymorphism and are developed by a combination of restriction endonuclease digestion and Southern blotting hybridization. CAPS are similarly developed from restriction

10   nuclease digestion but only of specific PCR products. These markers are also codominant, have a medium level of polymorphism and are highly abundant in the genome. The CAPS result from single base changes and insertions/deletions.

Another marker type, RAPDs, are developed from DNA amplification with random primers and result from single base changes and insertions/deletions in plant genomes. They are

15   dominant markers with a medium level of polymorphisms and are highly abundant. AFLP markers require using the PCR on a subset of restriction fragments from extended adapter primers. These markers are both dominant and codominant are highly abundant in genomes and exhibit a medium level of polymorphism.

SSRs require DNA sequence information. These codominant markers result from repeat

20   length changes, are highly polymorphic and do not exhibit as high a degree of abundance in the genome as CAPS, AFLPs and RAPDs SNPs also require DNA sequence information. These codominant markers result from single base substitutions. They are highly abundant and exhibit a medium of polymorphism (Rafalski *et al.*, In: *Nonmammalian Genomic Analysis*, Birren and

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Lai (ed.), Academic Press, San Diego, CA, pp. 75-134 (1996), the entirety of which is herein incorporated by reference). It is understood that a nucleic acid molecule of the present invention may be used as a marker.

A PCR probe is a nucleic acid molecule capable of initiating a polymerase activity while in a double-stranded structure to with another nucleic acid. Various methods for determining the structure of PCR probes and PCR techniques exist in the art. Computer generated searches using programs such as Primer3 (www-genome.wi.mit.edu/cgi-bin/primer/primer3.cgi), STSPipeline (www-genome.wi.mit.edu/cgi-bin/www-STS_Pipeline), or GeneUp (Pesole *et al.*, *BioTechniques 25*:112-123 (1998) the entirety of which is herein incorporated by reference), for example, can be used to identify potential PCR primers.

It is understood that a fragment of one or more of the nucleic acid molecules of the present invention may be a probe and specifically a PCR probe.

(b)   Protein and Peptide Molecules

A class of agents comprises one or more of the protein or fragments thereof or peptide molecules encoded by SEQ ID NO: 1 through SEQ ID NO: 699 or one or more of the protein or fragment thereof and peptide molecules encoded by other nucleic acid agents of the present invention. As used herein, the term "protein molecule" or "peptide molecule" includes any molecule that comprises five or more amino acids. It is well known in the art that proteins may undergo modification, including post-translational modifications, such as, but not limited to, disulfide bond formation, glycosylation, phosphorylation, or oligomerization. Thus, as used herein, the term "protein molecule" or "peptide molecule" includes any protein molecule that is modified by any biological or non-biological process. The terms "amino acid" and "amino

acids" refer to all naturally occurring L-amino acids. This definition is meant to include

norleucine, ornithine, homocysteine and homoserine.

Non-limiting examples of the protein or fragment thereof of the present invention include

a maize or soybean phosphogluconate pathway enzyme or fragment thereof; a maize or soybean

5   glucose-6-phosphate-1-dehydrogenase enzyme or fragment thereof; a maize or soybean 6-

phosphogluconate dehydrogenase enzyme or fragment thereof; a putative maize or soybean 6-

phosphogluconate dehydrogenase enzyme or fragment thereof; a maize or soybean D-ribulose-5-

phosphate-3-epimerase enzyme or fragment thereof; a maize or soybean ribose-5-phosphate

isomerase enzyme or fragment thereof; a putative maize or soybean ribose-5-phosphate

10   isomerase enzyme or fragment thereof; a maize or soybean transketolase enzyme or fragment

thereof; a putative maize or soybean transketolase enzyme or fragment thereof; a maize or

soybean transaldolase enzyme or fragment thereof; a putative maize transaldolase enzyme or

fragment thereof; and a maize or soybean phosphoglucoisomerase enzyme or fragment thereof.

Non-limiting examples of the protein or fragment molecules of the present invention are a

15   phosphogluconate pathway enzyme or fragment thereof encoded by: SEQ ID NO: 1 through

SEQ ID NO: 699 or fragment thereof that encode for a phosphogluconate pathway enzyme or

fragment thereof, SEQ ID NO: 1 through SEQ ID NO: 3 and SEQ ID NO: 4 through SEQ ID

NO: 11 or fragment thereof that encodes for a maize or soybean glucose-6-phosphate-1-

dehydrogenase enzyme or fragment thereof; SEQ ID NO: 12 through SEQ ID NO: 21 and SEQ

20   ID NO: 22 through SEQ ID NO: 103 or fragment thereof that encodes for a maize or soybean 6-

phosphogluconate dehydrogenase enzyme or fragment thereof; SEQ ID NO: 104 through SEQ

ID NO: 209 and SEQ ID NO: 210 through SEQ ID NO: 214 or fragment thereof that encodes for

a putative maize or soybean 6-phosphogluconate dehydrogenase enzyme or fragment thereof;

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SEQ ID NO: 215 through SEQ ID NO: 260 and SEQ ID NO: 261 through SEQ ID NO: 299 or

fragment thereof that encodes for a putative maize or soybean D-ribulose-5-phosphate-3-

epimerase enzyme or fragment thereof; SEQ ID NO: 300 through SEQ ID NO: 306 and SEQ ID

NO: 307 through SEQ ID NO: 311 or fragment thereof that encodes for a maize or soybean

5   ribose-5-phosphate isomerase enzyme or fragment thereof; SEQ ID NO: 312 through SEQ ID

NO: 313 and SEQ ID NO: 314 through SEQ ID NO: 318 or fragment thereof that encodes for a

putaive maize or soybean ribose-5-phosphate isomerase enzyme or fragment thereof; SEQ ID

NO: 319 through SEQ ID NO: 356 and SEQ ID NO: 357 through SEQ ID NO: 437 or fragment

thereof that encodes for a maize or soybean transketolase enzyme or fragment thereof; SEQ ID

10   NO: 438 through SEQ ID NO: 447 and SEQ ID NO: 448 through SEQ ID NO: 453 or fragment

thereof that encodes for a putative maize or soybean transketolase enzyme or fragment thereof;

SEQ ID NO: 454 through SEQ ID NO: 533 and SEQ ID NO: 534 through SEQ ID NO: 617 or

fragment thereof that encodes for a maize or a soybean transaldolase enzyme or fragment thereof;

SEQ ID NO: 618 or fragment thereof that encode for a putative maize transaldolase enzyme or

15   fragment thereof; and SEQ ID NO: 619 through SEQ ID NO: 683 and SEQ ID NO: 684 through

SEQ ID NO: 699 or fragment thereof that encodes for a maize or soybean

phosphoglucoisomerase enzyme or fragment thereof.

One or more of the protein or fragment of peptide molecules may be produced via

chemical synthesis, or more preferably, by expressing in a suitable bacterial or eucaryotic host.

20   Suitable methods for expression are described by Sambrook *et al.*, (In: *Molecular Cloning, A*

Laboratory Manual, 2nd Edition, Cold Spring Harbor Press, Cold Spring Harbor, New York

(1989)), or similar texts. For example, the protein may be expressed in, for example, Uses of the

Agents of the Invention, Section (a) Plant Constructs and Plant Transformants; Section (b)

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Fungal Constructs and Fungal Transformants; Section (c) Mammalian Constructs and Transformed Mammalian Cells; Section (d) Insect Constructs and Transformed Insect Cells; and Section (e) Bacterial Constructs and Transformed Bacterial Cells.

A "protein fragment" is a peptide or polypeptide molecule whose amino acid sequence comprises a subset of the amino acid sequence of that protein. A protein or fragment thereof that comprises one or more additional peptide regions not derived from that protein is a "fusion" protein. Such molecules may be derivatized to contain carbohydrate or other moieties (such as keyhole limpet hemocyanin, etc.). Fusion protein or peptide molecules of the present invention are preferably produced via recombinant means.

Another class of agents comprise protein or peptide molecules or fragments or fusions thereof encoded by SEQ ID NO: 1 through SEQ ID NO: 699 or complements thereof in which conservative, non-essential or non-relevant amino acid residues have been added, replaced or deleted. Computerized means for designing modifications in protein structure are known in the art (Dahiyat and Mayo, *Science* 278:82-87 (1997), the entirety of which is herein incorporated by reference).

The protein molecules of the present invention include plant homologue proteins. An example of such a homologue is a homologue protein of a non-maize or non-soybean plant species, that include but not limited to alfalfa, *Arabidopsis*, barley, *Brassica*, broccoli, cabbage, citrus, cotton, garlic, oat, oilseed rape, onion, canola, flax, an ornamental plant, pea, peanut, pepper, potato, rice, rye, sorghum, strawberry, sugarcane, sugarbeet, tomato, wheat, poplar, pine, fir, eucalyptus, apple, lettuce, lentils, grape, banana, tea, turf grasses, sunflower, oil palm, *Phaseolus* etc. Particularly preferred non-maize or non-soybean for use for the isolation of homologs would include, *Arabidopsis,* barley, cotton, oat, oilseed rape, rice, canola, ornamentals,

sugarcane, sugarbeet, tomato, potato, wheat and turf grasses. Such a homologue can be obtained

by any of a variety of methods. Most preferably, as indicated above, one or more of the

disclosed sequences (SEQ ID NO: 1 through SEQ ID NO: 699 or complements thereof) will be

used to define a pair of primers that may be used to isolate the homologue-encoding nucleic acid

5   molecules from any desired species. Such molecules can be expressed to yield homologues by

recombinant means.

(c) Antibodies

One aspect of the present invention concerns antibodies, single-chain antigen binding

molecules, or other proteins that specifically bind to one or more of the protein or peptide

10   molecules of the present invention and their homologues, fusions or fragments. Such antibodies

may be used to quantitatively or qualitatively detect the protein or peptide molecules of the

present invention. As used herein, an antibody or peptide is said to "specifically bind" to a

protein or peptide molecule of the present invention if such binding is not competitively inhibited

by the presence of non-related molecules.

15   Nucleic acid molecules that encode all or part of the protein of the present invention can

be expressed, via recombinant means, to yield protein or peptides that can in turn be used to elicit

antibodies that are capable of binding the expressed protein or peptide. Such antibodies may be

used in immunoassays for that protein. Such protein-encoding molecules, or their fragments may

be a "fusion" molecule (i.e., a part of a larger nucleic acid molecule) such that, upon expression,

20   a fusion protein is produced. It is understood that any of the nucleic acid molecules of the

present invention may be expressed, via recombinant means, to yield proteins or peptides

encoded by these nucleic acid molecules.

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The antibodies that specifically bind proteins and protein fragments of the present

invention may be polyclonal or monoclonal and may comprise intact immunoglobulins, or

antigen binding portions of immunoglobulins fragments (such as (F(ab'), F(ab')$_2$), or single-chain

immunoglobulins producible, for example, via recombinant means. It is understood that

5   practitioners are familiar with the standard resource materials which describe specific conditions

and procedures for the construction, manipulation and isolation of antibodies (*see*, for example,

Harlow and Lane, In: *Antibodies: A Laboratory Manual,* Cold Spring Harbor Press, Cold Spring

Harbor, New York (1988), the entirety of which is herein incorporated by reference).

Murine monoclonal antibodies are particularly preferred. BALB/c mice are preferred for

10   this purpose, however, equivalent strains may also be used. The animals are preferably

immunized with approximately 25 µg of purified protein (or fragment thereof) that has been

emulsified in a suitable adjuvant (such as TiterMax adjuvant (Vaxcel, Norcross, GA)).

Immunization is preferably conducted at two intramuscular sites, one intraperitoneal site and one

subcutaneous site at the base of the tail. An additional i.v. injection of approximately 25 µg of

15   antigen is preferably given in normal saline three weeks later. After approximately 11 days

following the second injection, the mice may be bled and the blood screened for the presence of

anti-protein or peptide antibodies. Preferably, a direct binding Enzyme-Linked Immunoassay

(ELISA) is employed for this purpose.

More preferably, the mouse having the highest antibody titer is given a third i.v. injection

20   of approximately 25 µg of the same protein or fragment. The splenic leukocytes from this

animal may be recovered 3 days later and then permitted to fuse, most preferably, using

polyethylene glycol, with cells of a suitable myeloma cell line (such as, for example, the

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P3X63Ag8.653 myeloma cell line). Hybridoma cells are selected by culturing the cells under

"HAT" (hypoxanthine-aminopterin-thymine) selection for about one week. The resulting clones

may then be screened for their capacity to produce monoclonal antibodies ("mAbs"), preferably

by direct ELISA.

In one embodiment, anti-protein or peptide monoclonal antibodies are isolated using a

fusion of a protein or peptide of the present invention, or conjugate of a protein or peptide of the

present invention, as immunogens. Thus, for example, a group of mice can be immunized using

a fusion protein emulsified in Freund's complete adjuvant (e.g. approximately 50 µg of antigen

per immunization). At three week intervals, an identical amount of antigen is emulsified in

Freund's incomplete adjuvant and used to immunize the animals. Ten days following the third

immunization, serum samples are taken and evaluated for the presence of antibody. If antibody

titers are too low, a fourth booster can be employed. Polysera capable of binding the protein or

peptide can also be obtained using this method.

In a preferred procedure for obtaining monoclonal antibodies, the spleens of the above-

described immunized mice are removed, disrupted and immune splenocytes are isolated over a

ficoll gradient. The isolated splenocytes are fused, using polyethylene glycol with BALB/c-

derived HGPRT (hypoxanthine guanine phosphoribosyl transferase) deficient P3x63xAg8.653

plasmacytoma cells. The fused cells are plated into 96 well microtiter plates and screened for

hybridoma fusion cells by their capacity to grow in culture medium supplemented with

hypothanthine, aminopterin and thymidine for approximately 2-3 weeks.

Hybridoma cells that arise from such incubation are preferably screened for their capacity

to produce an immunoglobulin that binds to a protein of interest. An indirect ELISA may be

used for this purpose. In brief, the supernatants of hybridomas are incubated in microtiter wells

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that contain immobilized protein. After washing, the titer of bound immunoglobulin can be determined using, for example, a goat anti-mouse antibody conjugated to horseradish peroxidase. After additional washing, the amount of immobilized enzyme is determined (for example through the use of a chromogenic substrate). Such screening is performed as quickly as possible

5   after the identification of the hybridoma in order to ensure that a desired clone is not overgrown by non-secreting neighbor cells. Desirably, the fusion plates are screened several times since the rates of hybridoma growth vary. In a preferred sub-embodiment, a different antigenic form may be used to screen the hybridoma. Thus, for example, the splenocytes may be immunized with one immunogen, but the resulting hybridomas can be screened using a different immunogen. It

10   is understood that any of the protein or peptide molecules of the present invention may be used to raise antibodies.

As discussed below, such antibody molecules or their fragments may be used for diagnostic purposes. Where the antibodies are intended for diagnostic purposes, it may be desirable to derivatize them, for example with a ligand group (such as biotin) or a detectable

15   marker group (such as a fluorescent group, a radioisotope or an enzyme).

The ability to produce antibodies that bind the protein or peptide molecules of the present invention permits the identification of mimetic compounds of those molecules. A "mimetic compound" is a compound that is not that compound, or a fragment of that compound, but which nonetheless exhibits an ability to specifically bind to antibodies directed against that compound.

20   It is understood that any of the agents of the present invention can be substantially purified and/or be biologically active and/or recombinant.

Uses of the Agents of the Invention

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Nucleic acid molecules and fragments thereof of the present invention may be employed to obtain other nucleic acid molecules from the same species (e.g., ESTs or fragment thereof from maize may be utilized to obtain other nucleic acid molecules from maize). Such nucleic acid molecules include the nucleic acid molecules that encode the complete coding sequence of a protein and promoters and flanking sequences of such molecules. In addition, such nucleic acid molecules include nucleic acid molecules that encode for other isozymes or gene family members. Such molecules can be readily obtained by using the above-described nucleic acid molecules or fragments thereof to screen cDNA or genomic libraries obtained from maize or soybean. Methods for forming such libraries are well known in the art.

Nucleic acid molecules and fragments thereof of the present invention may also be employed to obtain nucleic acid homologues. Such homologues include the nucleic acid molecule of other plants or other organisms (*e.g.*, alfalfa, *Arabidopsis*, barley, *Brassica*, broccoli, cabbage, citrus, cotton, garlic, oat, oilseed rape, onion, canola, flax, an ornamental plant, pea, peanut, pepper, potato, rice, rye, sorghum, strawberry, sugarcane, sugarbeet, tomato, wheat, poplar, pine, fir, eucalyptus, apple, lettuce, lentils, grape, banana, tea, turf grasses, sunflower, oil palm, *Phaseolus,* etc.) including the nucleic acid molecules that encode, in whole or in part, protein homologues of other plant species or other organisms, sequences of genetic elements such as promoters and transcriptional regulatory elements. Such molecules can be readily obtained by using the above-described nucleic acid molecules or fragments thereof to screen cDNA or genomic libraries obtained from such plant species. Methods for forming such libraries are well known in the art. Such homologue molecules may differ in their nucleotide sequences from those found in one or more of SEQ ID NO: 1 through SEQ ID NO: 699 or complements thereof because complete complementarity is not needed for stable hybridization. The nucleic

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acid molecules of the present invention therefore also include molecules that, although capable of specifically hybridizing with the nucleic acid molecules may lack "complete complementarity."

Any of a variety of methods may be used to obtain one or more of the above-described nucleic acid molecules (Zamechik et al., Proc. Natl. Acad. Sci. (U.S.A.) 83:4143-4146 (1986),

5   the entirety of which is herein incorporated by reference; Goodchild et al., Proc. Natl. Acad. Sci. (U.S.A.) 85:5507-5511 (1988), the entirety of which is herein incorporated by reference; Wickstrom et al., Proc. Natl. Acad. Sci. (U.S.A.) 85:1028-1032 (1988), the entirety of which is herein incorporated by reference; Holt et al., Molec. Cell. Biol. 8:963-973 (1988), the entirety of which is herein incorporated by reference; Gerwirtz et al., Science 242:1303-1306 (1988), the

10   entirety of which is herein incorporated by reference; Anfossi et al., Proc. Natl. Acad. Sci. (U.S.A.) 86:3379-3383 (1989), the entirety of which is herein incorporated by reference; Becker et al., EMBO J. 8:3685-3691 (1989); the entirety of which is herein incorporated by reference). Automated nucleic acid synthesizers may be employed for this purpose. In lieu of such synthesis, the disclosed nucleic acid molecules may be used to define a pair of primers that can

15   be used with the polymerase chain reaction (Mullis et al., Cold Spring Harbor Symp. Quant. Biol. 51:263-273 (1986); Erlich et al., European Patent 50,424; European Patent 84,796; European Patent 258,017; European Patent 237,362; Mullis, European Patent 201,184; Mullis et al., U.S. Patent No. 4,683,202; Erlich, U.S. Patent No. 4,582,788; and Saiki et al., U.S. Patent No. 4,683,194, all of which are herein incorporated by reference in their entirety) to amplify and

20   obtain any desired nucleic acid molecule or fragment.

Promoter sequence(s) and other genetic elements, including but not limited to transcriptional regulatory flanking sequences, associated with one or more of the disclosed nucleic acid sequences can also be obtained using the disclosed nucleic acid sequence provided

herein. In one embodiment, such sequences are obtained by incubating EST nucleic acid molecules or preferably fragments thereof with members of genomic libraries (*e.g.* maize and soybean) and recovering clones that hybridize to the EST nucleic acid molecule or fragment thereof. In a second embodiment, methods of "chromosome walking," or inverse PCR may be used to obtain such sequences (Frohman *et al.*, *Proc. Natl. Acad. Sci. (U.S.A.)* 85:8998-9002 (1988); Ohara *et al.*, *Proc. Natl. Acad. Sci. (U.S.A.)* 86:5673-5677 (1989); Pang *et al.*, *Biotechniques* 22:1046-1048 (1977); Huang *et al.*, *Methods Mol. Biol.* 69:89-96 (1997); Huang *et al.*, *Method Mol. Biol.* 67:287-294 (1997); Benkel *et al.*, *Genet. Anal.* 13:123-127 (1996); Hartl *et al.*, *Methods Mol. Biol.* 58:293-301 (1996), all of which are herein incorporated by reference in their entirety).

The nucleic acid molecules of the present invention may be used to isolate promoters of cell enhanced, cell specific, tissue enhanced, tissue specific, developmentally or environmentally regulated expression profiles. Isolation and functional analysis of the 5' flanking promoter sequences of these genes from genomic libraries, for example, using genomic screening methods and PCR techniques would result in the isolation of useful promoters and transcriptional regulatory elements. These methods are known to those of skill in the art and have been described (See, for example, Birren *et al.*, *Genome Analysis: Analyzing DNA*, 1, (1997), Cold Spring Harbor Laboratory Press, Cold Spring Harbor, N.Y., the entirety of which is herein incorporated by reference). Promoters obtained utilizing the nucleic acid molecules of the present invention could also be modified to affect their control characteristics. Examples of such modifications would include but are not limited to enhanced sequences as reported in Uses of the Agents of the Invention, Section (a) Plant Constructs and Plant Transformants. Such genetic

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elements could be used to enhance gene expression of new and existing traits for crop improvements.

In one sub-aspect, such an analysis is conducted by determining the presence and/or identity of polymorphism(s) by one or more of the nucleic acid molecules of the present invention and more preferably one or more of the EST nucleic acid molecule or fragment thereof which are associated with a phenotype, or a predisposition to that phenotype.

Any of a variety of molecules can be used to identify such polymorphism(s). In one embodiment, one or more of the EST nucleic acid molecules (or a sub-fragment thereof) may be employed as a marker nucleic acid molecule to identify such polymorphism(s). Alternatively, such polymorphisms can be detected through the use of a marker nucleic acid molecule or a marker protein that is genetically linked to (i.e., a polynucleotide that co-segregates with) such polymorphism(s).

In an alternative embodiment, such polymorphisms can be detected through the use of a marker nucleic acid molecule that is physically linked to such polymorphism(s). For this purpose, marker nucleic acid molecules comprising a nucleotide sequence of a polynucleotide located within 1mb of the polymorphism(s) and more preferably within 100kb of the polymorphism(s) and most preferably within 10kb of the polymorphism(s) can be employed.

The genomes of animals and plants naturally undergo spontaneous mutation in the course of their continuing evolution (Gusella, *Ann. Rev. Biochem.* *55*:831-854 (1986)). A "polymorphism" is a variation or difference in the sequence of the gene or its flanking regions that arises in some of the members of a species. The variant sequence and the "original" sequence co-exist in the species' population. In some instances, such co-existence is in stable or quasi-stable equilibrium.

A polymorphism is thus said to be "allelic," in that, due to the existence of the polymorphism, some members of a species may have the original sequence (i.e., the original "allele") whereas other members may have the variant sequence (i.e., the variant "allele"). In the simplest case, only one variant sequence may exist and the polymorphism is thus said to be di-

5   allelic. In other cases, the species' population may contain multiple alleles and the polymorphism is termed tri-allelic, etc. A single gene may have multiple different unrelated polymorphisms. For example, it may have a di-allelic polymorphism at one site and a multi-allelic polymorphism at another site.

The variation that defines the polymorphism may range from a single nucleotide variation

10   to the insertion or deletion of extended regions within a gene. In some cases, the DNA sequence variations are in regions of the genome that are characterized by short tandem repeats (STRs) that include tandem di- or tri-nucleotide repeated motifs of nucleotides. Polymorphisms characterized by such tandem repeats are referred to as "variable number tandem repeat" ("VNTR") polymorphisms. VNTRs have been used in identity analysis (Weber, U.S. Patent No.

15   5,075,217; Armour et al., FEBS Lett. 307:113-115 (1992); Jones et al., Eur. J. Haematol. 39:144-147 (1987); Horn et al., PCT Patent Application WO91/14003; Jeffreys, European Patent Application 370,719; Jeffreys, U.S. Patent No. 5,175,082; Jeffreys et al., Amer. J. Hum. Genet. 39:11-24 (1986); Jeffreys et al., Nature 316:76-79 (1985); Gray et al., Proc. R. Acad. Soc. Lond. 243:241-253 (1991); Moore et al., Genomics 10:654-660 (1991); Jeffreys et al., Anim. Genet.

20   18:1-15 (1987); Hillel et al., Anim. Genet. 20:145-155 (1989); Hillel et al., Genet. 124:783-789 (1990), all of which are herein incorporated by reference in their entirety).

The detection of polymorphic sites in a sample of DNA may be facilitated through the use of nucleic acid amplification methods. Such methods specifically increase the concentration

of polynucleotides that span the polymorphic site, or include that site and sequences located either distal or proximal to it. Such amplified molecules can be readily detected by gel electrophoresis or other means.

The most preferred method of achieving such amplification employs the polymerase

5   chain reaction ("PCR") (Mullis *et al., Cold Spring Harbor Symp. Quant. Biol. 51*:263-273 (1986); Erlich *et al.*, European Patent Appln. 50,424; European Patent Appln. 84,796; European Patent Application 258,017; European Patent Appln. 237,362; Mullis, European Patent Appln. 201,184; Mullis *et al.*, U.S. Patent No. 4,683,202; Erlich, U.S. Patent No. 4,582,788; and Saiki *et al.*, U.S. Patent No. 4,683,194), using primer pairs that are capable of hybridizing to the proximal

10 sequences that define a polymorphism in its double-stranded form.

In lieu of PCR, alternative methods, such as the "Ligase Chain Reaction" ("LCR") may be used (Barany, *Proc. Natl. Acad. Sci. (U.S.A.) 88*:189-193 (1991), the entirety of which is herein incorporated by reference). LCR uses two pairs of oligonucleotide probes to exponentially amplify a specific target. The sequences of each pair of oligonucleotides is

15 selected to permit the pair to hybridize to abutting sequences of the same strand of the target. Such hybridization forms a substrate for a template-dependent ligase. As with PCR, the resulting products thus serve as a template in subsequent cycles and an exponential amplification of the desired sequence is obtained.

LCR can be performed with oligonucleotides having the proximal and distal sequences of

20 the same strand of a polymorphic site. In one embodiment, either oligonucleotide will be designed to include the actual polymorphic site of the polymorphism. In such an embodiment, the reaction conditions are selected such that the oligonucleotides can be ligated together only if the target molecule either contains or lacks the specific nucleotide that is complementary to the

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polymorphic site present on the oligonucleotide. Alternatively, the oligonucleotides may be selected such that they do not include the polymorphic site (see, Segev, PCT Application WO 90/01069, the entirety of which is herein incorporated by reference).

The "Oligonucleotide Ligation Assay" ("OLA") may alternatively be employed (Landegren *et al.*, *Science 241*:1077-1080 (1988), the entirety of which is herein incorporated by reference). The OLA protocol uses two oligonucleotides which are designed to be capable of hybridizing to abutting sequences of a single strand of a target. OLA, like LCR, is particularly suited for the detection of point mutations. Unlike LCR, however, OLA results in "linear" rather than exponential amplification of the target sequence.

Nickerson *et al.*, have described a nucleic acid detection assay that combines attributes of PCR and OLA (Nickerson *et al.*, *Proc. Natl. Acad. Sci. (U.S.A.) 87*:8923-8927 (1990), the entirety of which is herein incorporated by reference). In this method, PCR is used to achieve the exponential amplification of target DNA, which is then detected using OLA. In addition to requiring multiple and separate, processing steps, one problem associated with such combinations is that they inherit all of the problems associated with PCR and OLA.

Schemes based on ligation of two (or more) oligonucleotides in the presence of nucleic acid having the sequence of the resulting "di-oligonucleotide", thereby amplifying the di-oligonucleotide, are also known (Wu *et al.*, *Genomics 4*:560-569 (1989), the entirety of which is herein incorporated by reference) and may be readily adapted to the purposes of the present invention.

Other known nucleic acid amplification procedures, such as allele-specific oligomers, branched DNA technology, transcription-based amplification systems, or isothermal amplification methods may also be used to amplify and analyze such polymorphisms (Malek *et*

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al., U.S. Patent No. 5,130,238; Davey *et al.*, European Patent Application 329,822; Schuster *et al.*, U.S. Patent No. 5,169,766; Miller *et al.*, PCT Patent Application WO 89/06700; Kwoh *et al.*, *Proc. Natl. Acad. Sci. (U.S.A.)* 86:1173-1177 (1989); Gingeras *et al.*, PCT Patent Application WO 88/10315; Walker *et al.*, *Proc. Natl. Acad. Sci. (U.S.A.)* 89:392-396 (1992), all of which are

5   herein incorporated by reference in their entirety).

The identification of a polymorphism can be determined in a variety of ways. By correlating the presence or absence of it in a plant with the presence or absence of a phenotype, it is possible to predict the phenotype of that plant. If a polymorphism creates or destroys a restriction endonuclease cleavage site, or if it results in the loss or insertion of DNA (e.g., a

10   VNTR polymorphism), it will alter the size or profile of the DNA fragments that are generated by digestion with that restriction endonuclease. As such, individuals that possess a variant sequence can be distinguished from those having the original sequence by restriction fragment analysis. Polymorphisms that can be identified in this manner are termed "restriction fragment length polymorphisms" ("RFLPs"). RFLPs have been widely used in human and plant genetic

15   analyses (Glassberg, UK Patent Application 2135774; Skolnick *et al.*, *Cytogen. Cell Genet.* 32:58-67 (1982); Botstein *et al.*, *Ann. J. Hum. Genet.* 32:314-331 (1980); Fischer *et al.*, (PCT Application WO90/13668); Uhlen, PCT Application WO90/11369).

Polymorphisms can also be identified by Single Strand Conformation Polymorphism (SSCP) analysis. SSCP is a method capable of identifying most sequence variations in a single

20   strand of DNA, typically between 150 and 250 nucleotides in length (Elles, *Methods in Molecular Medicine: Molecular Diagnosis of Genetic Diseases*, Humana Press (1996), the entirety of which is herein incorporated by reference); Orita *et al.*, *Genomics 5:*874-879 (1989), the entirety of which is herein incorporated by reference). Under denaturing conditions a single

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strand of DNA will adopt a conformation that is uniquely dependent on its sequence conformation. This conformation usually will be different, even if only a single base is changed. Most conformations have been reported to alter the physical configuration or size sufficiently to be detectable by electrophoresis. A number of protocols have been described for SSCP

5   including, but not limited to, Lee *et al.*, *Anal. Biochem.* *205*:289-293 (1992), the entirety of which is herein incorporated by reference; Suzuki *et al.*, *Anal. Biochem.* *192*:82-84 (1991), the entirety of which is herein incorporated by reference; Lo *et al.*, *Nucleic Acids Research 20*:1005-1009 (1992), the entirety of which is herein incorporated by reference; Sarkar *et al.*, *Genomics 13*:441-443 (1992), the entirety of which is herein incorporated by reference. It is understood

10   that one or more of the nucleic acids of the present invention, may be utilized as markers or probes to detect polymorphisms by SSCP analysis.

Polymorphisms may also be found using a DNA fingerprinting technique called amplified fragment length polymorphism (AFLP), which is based on the selective PCR amplification of restriction fragments from a total digest of genomic DNA to profile that DNA

15   (Vos *et al.*, *Nucleic Acids Res.* *23*:4407-4414 (1995), the entirety of which is herein incorporated by reference). This method allows for the specific co-amplification of high numbers of restriction fragments, which can be visualized by PCR without knowledge of the nucleic acid sequence.

AFLP employs basically three steps. Initially, a sample of genomic DNA is cut with

20   restriction enzymes and oligonucleotide adapters are ligated to the restriction fragments of the DNA. The restriction fragments are then amplified using PCR by using the adapter and restriction sequence as target sites for primer annealing. The selective amplification is achieved by the use of primers that extend into the restriction fragments, amplifying only those fragments

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in which the primer extensions match the nucleotide flanking the restriction sites. These

amplified fragments are then visualized on a denaturing polyacrylamide gel.

AFLP analysis has been performed on *Salix* (Beismann *et al.*, *Mol. Ecol.* 6:989-993

(1997), the entirety of which is herein incorporated by reference), *Acinetobacter* (Janssen *et al.*,

5   *Int. J. Syst. Bacteriol.* 47:1179-1187 (1997), the entirety of which is herein incorporated by

reference), *Aeromonas popoffi* (Huys *et al.*, *Int. J. Syst. Bacteriol.* 47:1165-1171 (1997), the

entirety of which is herein incorporated by reference), rice (McCouch *et al.*, *Plant Mol. Biol.*

35:89-99 (1997), the entirety of which is herein incorporated by reference; Nandi *et al.*, *Mol.*

Gen. Genet. 255:1-8 (1997), the entirety of which is herein incorporated by reference; Cho *et al.*,

10   *Genome* 39:373-378 (1996), the entirety of which is herein incorporated by reference), barley

(*Hordeum vulgare*)(Simons *et al.*, *Genomics* 44:61-70 (1997), the entirety of which is herein

incorporated by reference; Waugh *et al.*, *Mol. Gen. Genet.* 255:311-321 (1997), the entirety of

which is herein incorporated by reference; Qi *et al.*, *Mol. Gen Genet.* 254:330-336 (1997), the

entirety of which is herein incorporated by reference; Becker *et al.*, *Mol. Gen. Genet.* 249:65-73

15   (1995), the entirety of which is herein incorporated by reference), potato (Van der Voort *et al.*,

Mol. Gen. Genet. 255:438-447 (1997), the entirety of which is herein incorporated by reference;

Meksem *et al.*, *Mol. Gen. Genet.* 249:74-81 (1995), the entirety of which is herein incorporated

by reference), *Phytophthora infestans* (Van der Lee *et al.*, *Fungal Genet. Biol.* 21:278-291

(1997), the entirety of which is herein incorporated by reference), *Bacillus anthracis* (Keim *et*

20   *al.*, *J. Bacteriol.* 179:818-824 (1997), the entirety of which is herein incorporated by reference),

Astragalus cremnophylax (Travis *et al.*, *Mol. Ecol.* 5:735-745 (1996), the entirety of which is

herein incorporated by reference), *Arabidopsis* (Cnops *et al.*, *Mol. Gen. Genet.* 253:32-41 (1996),

the entirety of which is herein incorporated by reference), *Escherichia coli* (Lin *et al.*, *Nucleic*

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Acids Res. *24*:3649-3650 (1996), the entirety of which is herein incorporated by reference),

Aeromonas (Huys *et al.*, *Int. J. Syst. Bacteriol.* *46*:572-580 (1996), the entirety of which is herein

incorporated by reference), nematode (Folkertsma *et al.*, *Mol. Plant Microbe Interact.* *9*:47-54

(1996), the entirety of which is herein incorporated by reference), tomato (Thomas *et al.*, *Plant J.*

5 *8*:785-794 (1995), the entirety of which is herein incorporated by reference) and human (Latorra

et al., *PCR Methods Appl.* *3*:351-358 (1994), the entirety of which is herein incorporated by

reference). AFLP analysis has also been used for fingerprinting mRNA (Money *et al.*, *Nucleic*

Acids Res. *24*:2616-2617 (1996), the entirety of which is herein incorporated by reference;

Bachem *et al.*, *Plant J.* *9*:745-753 (1996), the entirety of which is herein incorporated by

10 reference). It is understood that one or more of the nucleic acids of the present invention, may be

utilized as markers or probes to detect polymorphisms by AFLP analysis or for fingerprinting

RNA.

Polymorphisms may also be found using random amplified polymorphic DNA (RAPD)

(Williams *et al.*, *Nucl. Acids Res.* *18*:6531-6535 (1990), the entirety of which is herein

15 incorporated by reference) and cleaveable amplified polymorphic sequences (CAPS) (Lyamichev

et al., *Science* *260*:778-783 (1993), the entirety of which is herein incorporated by reference). It

is understood that one or more of the nucleic acid molecules of the present invention, may be

utilized as markers or probes to detect polymorphisms by RAPD or CAPS analysis.

Through genetic mapping, a fine scale linkage map can be developed using DNA markers

20 and, then, a genomic DNA library of large-sized fragments can be screened with molecular

markers linked to the desired trait. Molecular markers are advantageous for agronomic traits that

are otherwise difficult to tag, such as resistance to pathogens, insects and nematodes, tolerance to

abiotic stress, quality parameters and quantitative traits such as high yield potential.

The essential requirements for marker-assisted selection in a plant breeding program are: (1) the marker(s) should co-segregate or be closely linked with the desired trait; (2) an efficient means of screening large populations for the molecular marker(s) should be available; and (3) the screening technique should have high reproducibility across laboratories and preferably be economical to use and be user-friendly.

The genetic linkage of marker molecules can be established by a gene mapping model such as, without limitation, the flanking marker model reported by Lander and Botstein, *Genetics 121*:185-199 (1989) and the interval mapping, based on maximum likelihood methods described by Lander and Botstein, *Genetics 121*:185-199 (1989) and implemented in the software package MAPMAKER/QTL (Lincoln and Lander, *Mapping Genes Controlling Quantitative Traits Using MAPMAKER/QTL*, Whitehead Institute for Biomedical Research, Massachusetts, (1990). Additional software includes Qgene, Version 2.23 (1996), Department of Plant Breeding and Biometry, 266 Emerson Hall, Cornell University, Ithaca, NY, the manual of which is herein incorporated by reference in its entirety). Use of Qgene software is a particularly preferred approach.

A maximum likelihood estimate (MLE) for the presence of a marker is calculated, together with an MLE assuming no QTL effect, to avoid false positives. A $\log_{10}$ of an odds ratio (LOD) is then calculated as: LOD = $\log_{10}$ (MLE for the presence of a QTL/MLE given no linked QTL).

The LOD score essentially indicates how much more likely the data are to have arisen assuming the presence of a QTL than in its absence. The LOD threshold value for avoiding a false positive with a given confidence, say 95%, depends on the number of markers and the length of the genome. Graphs indicating LOD thresholds are set forth in Lander and Botstein,

Genetics 121:185-199 (1989) the entirety of which is herein incorporated by reference and further described by Arús and Moreno-González, *Plant Breeding*, Hayward *et al.*, (eds.) Chapman & Hall, London, pp. 314-331 (1993), the entirety of which is herein incorporated by reference.

5　　　　Additional models can be used. Many modifications and alternative approaches to interval mapping have been reported, including the use non-parametric methods (Kruglyak and Lander, *Genetics 139*:1421-1428 (1995), the entirety of which is herein incorporated by reference). Multiple regression methods or models can be also be used, in which the trait is regressed on a large number of markers (Jansen, *Biometrics in Plant Breeding*, van Oijen and Jansen (eds.), Proceedings of the Ninth Meeting of the Eucarpia Section Biometrics in Plant Breeding, The Netherlands, pp. 116-124 (1994); Weber and Wricke, *Advances in Plant Breeding*, Blackwell, Berlin, 16 (1994), both of which is herein incorporated by reference in their entirety). Procedures combining interval mapping with regression analysis, whereby the phenotype is regressed onto a single putative QTL at a given marker interval and at the same time onto a number of markers that serve as 'cofactors,' have been reported by Jansen and Stam, *Genetics 136*:1447-1455 (1994), the entirety of which is herein incorporated by reference and Zeng, *Genetics 136*:1457-1468 (1994) the entirety of which is herein incorporated by reference. Generally, the use of cofactors reduces the bias and sampling error of the estimated QTL positions (Utz and Melchinger, *Biometrics in Plant Breeding*, van Oijen and Jansen (eds.)

20　Proceedings of the Ninth Meeting of the Eucarpia Section Biometrics in Plant Breeding, The Netherlands, pp.195-204 (1994), the entirety of which is herein incorporated by reference, thereby improving the precision and efficiency of QTL mapping (Zeng, *Genetics 136*:1457-1468 (1994)). These models can be extended to multi-environment experiments to analyze genotype-

environment interactions (Jansen *et al., Theo. Appl. Genet. 91*:33-37 (1995), the entirety of which is herein incorporated by reference).

Selection of an appropriate mapping populations is important to map construction. The choice of appropriate mapping population depends on the type of marker systems employed (Tanksley *et al., Molecular mapping plant chromosomes. Chromosome structure and function: Impact of new concepts,* Gustafson and Appels (eds.), Plenum Press, New York, pp 157-173 (1988), the entirety of which is herein incorporated by reference). Consideration must be given to the source of parents (adapted vs. exotic) used in the mapping population. Chromosome pairing and recombination rates can be severely disturbed (suppressed) in wide crosses (adapted x exotic) and generally yield greatly reduced linkage distances. Wide crosses will usually provide segregating populations with a relatively large array of polymorphisms when compared to progeny in a narrow cross (adapted x adapted).

An F_2 population is the first generation of selfing after the hybrid seed is produced. Usually a single F_1 plant is selfed to generate a population segregating for all the genes in Mendelian (1:2:1) fashion. Maximum genetic information is obtained from a completely classified F_2 population using a codominant marker system (Mather, *Measurement of Linkage in Heredity,* Methuen and Co., (1938), the entirety of which is herein incorporated by reference). In the case of dominant markers, progeny tests (e.g. F_3, BCF_2) are required to identify the heterozygotes, thus making it equivalent to a completely classified F_2 population. However, this procedure is often prohibitive because of the cost and time involved in progeny testing. Progeny testing of F_2 individuals is often used in map construction where phenotypes do not consistently reflect genotype (e.g. disease resistance) or where trait expression is controlled by a QTL. Segregation data from progeny test populations (e.g. F_3 or BCF_2) can be used in map

construction. Marker-assisted selection can then be applied to cross progeny based on marker-trait map associations (F_2, F_3), where linkage groups have not been completely disassociated by recombination events (i.e., maximum disequillibrium).

Recombinant inbred lines (RIL) (genetically related lines; usually >F_5, developed from continuously selfing F_2 lines towards homozygosity) can be used as a mapping population. Information obtained from dominant markers can be maximized by using RIL because all loci are homozygous or nearly so. Under conditions of tight linkage (i.e., about <10% recombination), dominant and co-dominant markers evaluated in RIL populations provide more information per individual than either marker type in backcross populations (Reiter *et al.*, *Proc. Natl. Acad. Sci. (U.S.A.)* 89:1477-1481 (1992), the entirety of which is herein incorporated by reference). However, as the distance between markers becomes larger (i.e., loci become more independent), the information in RIL populations decreases dramatically when compared to codominant markers.

Backcross populations (e.g., generated from a cross between a successful variety (recurrent parent) and another variety (donor parent) carrying a trait not present in the former) can be utilized as a mapping population. A series of backcrosses to the recurrent parent can be made to recover most of its desirable traits. Thus a population is created consisting of individuals nearly like the recurrent parent but each individual carries varying amounts or mosaic of genomic regions from the donor parent. Backcross populations can be useful for mapping dominant markers if all loci in the recurrent parent are homozygous and the donor and recurrent parent have contrasting polymorphic marker alleles (Reiter *et al.*, *Proc. Natl. Acad. Sci. (U.S.A.)* 89:1477-1481 (1992)). Information obtained from backcross populations using either codominant or dominant markers is less than that obtained from F_2 populations because one,

rather than two, recombinant gametes are sampled per plant. Backcross populations, however, are more informative (at low marker saturation) when compared to RILs as the distance between linked loci increases in RIL populations (i.e. about 15% recombination). Increased recombination can be beneficial for resolution of tight linkages, but may be undesirable in the construction of maps with low marker saturation.

Near-isogenic lines (NIL) created by many backcrosses to produce an array of individuals that are nearly identical in genetic composition except for the trait or genomic region under interrogation can be used as a mapping population. In mapping with NILs, only a portion of the polymorphic loci are expected to map to a selected region.

Bulk segregant analysis (BSA) is a method developed for the rapid identification of linkage between markers and traits of interest (Michelmore *et al.*, *Proc. Natl. Acad. Sci. (U.S.A.)* *88*:9828-9832 (1991), the entirety of which is herein incorporated by reference). In BSA, two bulked DNA samples are drawn from a segregating population originating from a single cross. These bulks contain individuals that are identical for a particular trait (resistant or susceptible to particular disease) or genomic region but arbitrary at unlinked regions (i.e. heterozygous). Regions unlinked to the target region will not differ between the bulked samples of many individuals in BSA.

It is understood that one or more of the nucleic acid molecules of the present invention may be used as molecular markers. It is also understood that one or more of the protein molecules of the present invention may be used as molecular markers.

In accordance with this aspect of the present invention, a sample nucleic acid is obtained from plants cells or tissues. Any source of nucleic acid may be used. Preferably, the nucleic acid is genomic DNA. The nucleic acid is subjected to restriction endonuclease digestion. For

example, one or more nucleic acid molecule or fragment thereof of the present invention can be used as a probe in accordance with the above-described polymorphic methods. The polymorphism obtained in this approach can then be cloned to identify the mutation at the coding region which alters the protein's structure or regulatory region of the gene which affects its

5   expression level.

In an aspect of the present invention, one or more of the nucleic molecules of the present invention are used to determine the level (i.e., the concentration of mRNA in a sample, etc.) in a plant (preferably maize or soybean) or pattern (i.e., the kinetics of expression, rate of decomposition, stability profile, etc.) of the expression of a protein encoded in part or whole by

10   one or more of the nucleic acid molecule of the present invention (collectively, the "Expression Response" of a cell or tissue). As used herein, the Expression Response manifested by a cell or tissue is said to be "altered" if it differs from the Expression Response of cells or tissues of plants not exhibiting the phenotype. To determine whether an Expression Response is altered, the Expression Response manifested by the cell or tissue of the plant exhibiting the phenotype is

15   compared with that of a similar cell or tissue sample of a plant not exhibiting the phenotype. As will be appreciated, it is not necessary to re-determine the Expression Response of the cell or tissue sample of plants not exhibiting the phenotype each time such a comparison is made; rather, the Expression Response of a particular plant may be compared with previously obtained values of normal plants. As used herein, the phenotype of the organism is any of one or more

20   characteristics of an organism (e.g. disease resistance, pest tolerance, environmental tolerance such as tolerance to abiotic stress, male sterility, quality improvement or yield etc.). A change in genotype or phenotype may be transient or permanent. Also as used herein, a tissue sample is any sample that comprises more than one cell. In a preferred aspect, a tissue sample comprises

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cells that share a common characteristic (e.g. derived from root, seed, flower, leaf, stem or pollen etc.).

In one aspect of the present invention, an evaluation can be conducted to determine whether a particular mRNA molecule is present. One or more of the nucleic acid molecules of the present invention, preferably one or more of the EST nucleic acid molecules or fragments thereof of the present invention are utilized to detect the presence or quantity of the mRNA species. Such molecules are then incubated with cell or tissue extracts of a plant under conditions sufficient to permit nucleic acid hybridization. The detection of double-stranded probe-mRNA hybrid molecules is indicative of the presence of the mRNA; the amount of such hybrid formed is proportional to the amount of mRNA. Thus, such probes may be used to ascertain the level and extent of the mRNA production in a plant's cells or tissues. Such nucleic acid hybridization may be conducted under quantitative conditions (thereby providing a numerical value of the amount of the mRNA present). Alternatively, the assay may be conducted as a qualitative assay that indicates either that the mRNA is present, or that its level exceeds a user set, predefined value.

A principle of *in situ* hybridization is that a labeled, single-stranded nucleic acid probe will hybridize to a complementary strand of cellular DNA or RNA and, under the appropriate conditions, these molecules will form a stable hybrid. When nucleic acid hybridization is combined with histological techniques, specific DNA or RNA sequences can be identified within a single cell. An advantage of *in situ* hybridization over more conventional techniques for the detection of nucleic acids is that it allows an investigator to determine the precise spatial population (Angerer *et al., Dev. Biol. 101*:477-484 (1984), the entirety of which is herein incorporated by reference; Angerer *et al., Dev. Biol. 112*:157-166 (1985), the entirety of which is

herein incorporated by reference; Dixon *et al.*, *EMBO J. 10*:1317-1324 (1991), the entirety of

which is herein incorporated by reference). *In situ* hybridization may be used to measure the

steady-state level of RNA accumulation. It is a sensitive technique and RNA sequences present

in as few as 5-10 copies per cell can be detected (Hardin *et al.*, *J. Mol. Biol. 202*:417-431 (1989),

5   the entirety of which is herein incorporated by reference). A number of protocols have been

devised for *in situ* hybridization, each with tissue preparation, hybridization and washing

conditions (Meyerowitz, *Plant Mol. Biol. Rep. 5*:242-250 (1987), the entirety of which is herein

incorporated by reference; Cox and Goldberg, In: *Plant Molecular Biology: A Practical*

Approach, Shaw (ed.), pp 1-35, IRL Press, Oxford (1988), the entirety of which is herein

10   incorporated by reference; Raikhel *et al.*, *In situ RNA hybridization in plant tissues*, In: *Plant*

Molecular Biology Manual, vol. B9:1-32, Kluwer Academic Publisher, Dordrecht, Belgium

(1989), the entirety of which is herein incorporated by reference).

 In situ hybridization also allows for the localization of proteins within a tissue or cell

(Wilkinson, *In Situ Hybridization,* Oxford University Press, Oxford (1992), the entirety of which

15   is herein incorporated by reference; Langdale, *In Situ Hybridization* In: *The Maize Handbook,*

Freeling and Walbot (eds.), pp 165-179, Springer-Verlag, New York (1994), the entirety of

which is herein incorporated by reference). It is understood that one or more of the molecules of

the present invention, preferably one or more of the EST nucleic acid molecules or fragments

thereof of the present invention or one or more of the antibodies of the present invention may be

20   utilized to detect the level or pattern of a phosphogluconate pathway enzyme or mRNA thereof

by *in situ* hybridization.

 Fluorescent *in situ* hybridization allows the localization of a particular DNA sequence

along a chromosome which is useful, among other uses, for gene mapping, following

chromosomes in hybrid lines or detecting chromosomes with translocations, transversions or

deletions. *In situ* hybridization has been used to identify chromosomes in several plant species

(Griffor *et al.*, *Plant Mol. Biol. 17*:101-109 (1991), the entirety of which is herein incorporated

by reference; Gustafson *et al.*, *Proc. Natl. Acad. Sci. (U.S.A.) 87*:1899-1902 (1990), herein

5   incorporated by reference; Mukai and Gill, *Genome 34*:448-452 (1991), the entirety of which is

herein incorporated by reference; Schwarzacher and Heslop-Harrison, *Genome 34*:317-323

(1991); Wang *et al.*, *Jpn. J. Genet. 66*:313-316 (1991), the entirety of which is herein

incorporated by reference; Parra and Windle, *Nature Genetics 5*:17-21 (1993), the entirety of

which is herein incorporated by reference). It is understood that the nucleic acid molecules of the

10   present invention may be used as probes or markers to localize sequences along a chromosome.

Another method to localize the expression of a molecule is tissue printing. Tissue

printing provides a way to screen, at the same time on the same membrane many tissue sections

from different plants or different developmental stages. Tissue-printing procedures utilize films

designed to immobilize proteins and nucleic acids. In essence, a freshly cut section of a tissue is

15   pressed gently onto nitrocellulose paper, nylon membrane or polyvinylidene difluoride

membrane. Such membranes are commercially available (*e.g.* Millipore, Bedford, Massachusetts

U.S.A.). The contents of the cut cell transfer onto the membrane and the contents and are

immobilized to the membrane. The immobilized contents form a latent print that can be

visualized with appropriate probes. When a plant tissue print is made on nitrocellulose paper, the

20   cell walls leave a physical print that makes the anatomy visible without further treatment (Varner

and Taylor, *Plant Physiol. 91*:31-33 (1989), the entirety of which is herein incorporated by

reference).

Tissue printing on substrate films is described by Daoust, *Exp. Cell Res. 12*:203-211

(1957), the entirety of which is herein incorporated by reference, who detected amylase, protease,

ribonuclease and deoxyribonuclease in animal tissues using starch, gelatin and agar films. These

techniques can be applied to plant tissues (Yomo and Taylor, *Planta 112*:35-43 (1973); the

5   entirety of which is herein incorporated by reference; Harris and Chrispeels, *Plant Physiol.*

56:292-299 (1975), the entirety of which is herein incorporated by reference). Advances in

membrane technology have increased the range of applications of Daoust's tissue-printing

techniques allowing (Cassab and Varner, *J. Cell. Biol. 105*:2581-2588 (1987), the entirety of

which is herein incorporated by reference) the histochemical localization of various plant

10   enzymes and deoxyribonuclease on nitrocellulose paper and nylon (Spruce *et al.*, *Phytochemistry*

26:2901-2903 (1987), the entirety of which is herein incorporated by reference; Barres *et al.*,

Neuron 5:527-544 (1990), the entirety of which is herein incorporated by reference; Reid and

Pont-Lezica, *Tissue Printing: Tools for the Study of Anatomy, Histochemistry and Gene*

Expression, Academic Press, New York, New York (1992), the entirety of which is herein

15   incorporated by reference; Reid *et al.*, *Plant Physiol. 93*:160-165 (1990), the entirety of which is

herein incorporated by reference; Ye *et al.*, *Plant J. 1*:175-183 (1991), the entirety of which is

herein incorporated by reference).

It is understood that one or more of the molecules of the present invention, preferably one

or more of the EST nucleic acid molecules or fragments thereof of the present invention or one or

20   more of the antibodies of the present invention may be utilized to detect the presence or quantity

of a phosphogluconate pathway enzyme by tissue printing.

Further it is also understood that any of the nucleic acid molecules of the present

invention may be used as marker nucleic acids and or probes in connection with methods that

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require probes or marker nucleic acids. As used herein, a probe is an agent that is utilized to determine an attribute or feature (e.g. presence or absence, location, correlation, etc.) of a molecule, cell, tissue or plant. As used herein, a marker nucleic acid is a nucleic acid molecule that is utilized to determine an attribute or feature (*e.g.,* presence or absence, location,

5   correlation, etc.) or a molecule, cell, tissue or plant.

A microarray-based method for high-throughput monitoring of plant gene expression may be utilized to measure gene-specific hybridization targets. This 'chip'-based approach involves using microarrays of nucleic acid molecules as gene-specific hybridization targets to quantitatively measure expression of the corresponding plant genes (Schena *et al., Science*

10   *270*:467-470 (1995), the entirety of which is herein incorporated by reference; Shalon, Ph.D. Thesis, Stanford University (1996), the entirety of which is herein incorporated by reference). Every nucleotide in a large sequence can be queried at the same time. Hybridization can be used to efficiently analyze nucleotide sequences.

Several microarray methods have been described. One method compares the sequences

15   to be analyzed by hybridization to a set of oligonucleotides representing all possible subsequences (Bains and Smith, *J. Theor. Biol. 135*:303-307 (1989), the entirety of which is herein incorporated by reference). A second method hybridizes the sample to an array of oligonucleotide or cDNA molecules. An array consisting of oligonucleotides complementary to subsequences of a target sequence can be used to determine the identity of a target sequence,

20   measure its amount and detect differences between the target and a reference sequence. Nucleic acid molecule microarrays may also be screened with protein molecules or fragments thereof to determine nucleic acid molecules that specifically bind protein molecules or fragments thereof.

The microarray approach may be used with polypeptide targets (U.S. Patent No.

5,445,934; U.S. Patent No. 5,143,854; U.S. Patent No. 5,079,600; U.S. Patent No. 4,923,901, all

of which are herein incorporated by reference in their entirety). Essentially, polypeptides are

synthesized on a substrate (microarray) and these polypeptides can be screened with either

5   protein molecules or fragments thereof or nucleic acid molecules in order to screen for either

protein molecules or fragments thereof or nucleic acid molecules that specifically bind the target

polypeptides. (Fodor *et al.*, *Science 251*:767-773 (1991), the entirety of which is herein

incorporated by reference). It is understood that one or more of the nucleic acid molecules or

protein or fragments thereof of the present invention may be utilized in a microarray based

10   method.

In a preferred embodiment of the present invention microarrays may be prepared that

comprise nucleic acid molecules where such nucleic acid molecules encode at least one,

preferably at least two, more preferably at least three phosphogluconate pathway enzymes, more

preferably at least four phosphogluconate pathway enzymes, more preferably at least five

15   phosphogluconate pathway enzymes, more preferably at least six phosphogluconate pathway

enzymes, more preferably at least seven phosphogluconate pathway enzymes, more preferably at

least eight phosphogluconate pathway enzymes, more preferably at least nine phosphogluconate

pathway enzymes, more preferably at least ten phosphogluconate pathway enzymes, and even

more preferably at least eleven phosphogluconate pathway enzymes.

20   In a preferred embodiment the nucleic acid molecules are selected from the group

consisting of a nucleic acid molecule that encodes a maize or soybean glucose-6-phosphate-1-

dehydrogenase enzyme or fragment thereof; a nucleic acid molecule that encodes a maize or

soybean 6-phosphogluconate dehydrogenase enzyme or fragment thereof; a nucleic acid

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molecule that encodes a putative maize or soybean 6-phosphogluconate dehydrogenase enzyme or fragment thereof; a nucleic acid molecule that encodes a maize or soybean D-ribulose-5-phosphate-3-epimerase enzyme or fragment thereof; a nucleic acid molecule that encodes a maize or soybean ribose-5-phosphate isomerase enzyme or fragment thereof; a nucleic acid

5   molecule that encodes a putative maize or soybean ribose-5-phosphate isomerase enzyme or fragment thereof; a nucleic acid molecule that encodes a maize or soybean transketolase enzyme or fragment thereof; a nucleic acid molecule that encodes a putative maize or soybean transketolase enzyme or fragment thereof; a nucleic acid molecule that encodes a maize or soybean transaldolase enzyme or fragment thereof; a nucleic acid molecule that encodes a

10   putative maize transaldolase enzyme or fragment thereof; and a nucleic acid molecule that encodes a maize or soybean phosphoglucoisomerase enzyme or fragment thereof.

Site directed mutagenesis may be utilized to modify nucleic acid sequences, particularly as it is a technique that allows one or more of the amino acids encoded by a nucleic acid molecule to be altered (e.g. a threonine to be replaced by a methionine). Three basic methods for

15   site directed mutagenesis are often employed. These are cassette mutagenesis (Wells *et al.*, *Gene 34*:315-323 (1985), the entirety of which is herein incorporated by reference), primer extension (Gilliam *et al.*, *Gene 12*:129-137 (1980), the entirety of which is herein incorporated by reference; Zoller and Smith, *Methods Enzymol. 100*:468-500 (1983), the entirety of which is herein incorporated by reference; Dalbadie-McFarland *et al.*, *Proc. Natl. Acad. Sci. (U.S.A.)*

20   *79*:6409-6413 (1982), the entirety of which is herein incorporated by reference) and methods based upon PCR (Scharf *et al.*, *Science 233*:1076-1078 (1986), the entirety of which is herein incorporated by reference; Higuchi *et al.*, *Nucleic Acids Res. 16*:7351-7367 (1988), the entirety of which is herein incorporated by reference). Site directed mutagenesis approaches are also

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described in European Patent 0 385 962, the entirety of which is herein incorporated by reference; European Patent 0 359 472, the entirety of which is herein incorporated by reference; and PCT Patent Application WO 93/07278, the entirety of which is herein incorporated by reference.

5   Site directed mutagenesis strategies have been applied to plants for both *in vitro* as well as *in vivo* site directed mutagenesis (Lanz *et al.*, *J. Biol. Chem.* *266*:9971-9976 (1991), the entirety of which is herein incorporated by reference; Kovgan and Zhdanov, *Biotekhnologiya* *5*:148-154; No. 207160n, Chemical Abstracts 110:225 (1989), the entirety of which is herein incorporated by reference; Ge *et al.*, *Proc. Natl. Acad. Sci. (U.S.A.)* *86*:4037-4041 (1989), the entirety of which is herein incorporated by reference; Zhu *et al.*, *J. Biol. Chem.* *271*:18494-18498 (1996), the entirety of which is herein incorporated by reference; Chu *et al.*, *Biochemistry* *33*:6150-6157 (1994), the entirety of which is herein incorporated by reference; Small *et al.*, *EMBO J.* *11*:1291-1296 (1992), the entirety of which is herein incorporated by reference; Cho *et al.*, *Mol. Biotechnol.* *8*:13-16 (1997), the entirety of which is herein incorporated by reference; Kita *et al.*, *J. Biol. Chem.* *271*:26529-26535 (1996), the entirety of which is herein incorporated by reference, Jin *et al.*, *Mol. Microbiol.* *7*:555-562 (1993), the entirety of which is herein incorporated by reference; Hatfield and Vierstra, *J. Biol. Chem.* *267*:14799-14803 (1992), the entirety of which is herein incorporated by reference; Zhao *et al.*, *Biochemistry 31*:5093-5099 (1992), the entirety of which is herein incorporated by reference).

20   Any of the nucleic acid molecules of the present invention may either be modified by site directed mutagenesis or used as, for example, nucleic acid molecules that are used to target other nucleic acid molecules for modification. It is understood that mutants with more than one altered nucleotide can be constructed using techniques that practitioners are familiar with such as

isolating restriction fragments and ligating such fragments into an expression vector (*see,* for example, Sambrook *et al., Molecular Cloning: A Laboratory Manual,* Cold Spring Harbor Press (1989)).

Sequence-specific DNA-binding proteins play a role in the regulation of transcription. The isolation of recombinant cDNAs encoding these proteins facilitates the biochemical analysis of their structural and functional properties. Genes encoding such DNA-binding proteins have been isolated using classical genetics (Vollbrecht *et al., Nature 350*: 241-243 (1991), the entirety of which is herein incorporated by reference) and molecular biochemical approaches, including the screening of recombinant cDNA libraries with antibodies (Landschulz *et al., Genes Dev.* 2:786-800 (1988), the entirety of which is herein incorporated by reference) or DNA probes (Bodner *et al., Cell 55*:505-518 (1988), the entirety of which is herein incorporated by reference). In addition, an *in situ* screening procedure has been used and has facilitated the isolation of sequence-specific DNA-binding proteins from various plant species (Gilmartin *et al., Plant Cell* 4:839-849 (1992), the entirety of which is herein incorporated by reference; Schindler *et al., EMBO J. 11*:1261-1273 (1992), the entirety of which is herein incorporated by reference). An *in situ* screening protocol does not require the purification of the protein of interest (Vinson *et al., Genes Dev.* 2:801-806 (1988), the entirety of which is herein incorporated by reference; Singh *et al., Cell 52*:415-423 (1988), the entirety of which is herein incorporated by reference).

Two steps may be employed to characterize DNA-protein interactions. The first is to identify promoter fragments that interact with DNA-binding proteins, to titrate binding activity, to determine the specificity of binding and to determine whether a given DNA-binding activity can interact with related DNA sequences (Sambrook *et al., Molecular Cloning: A Laboratory Manual,* 2nd edition, Cold Spring Harbor Laboratory Press, Cold Spring Harbor, New York

(1989)). Electrophoretic mobility-shift assay is a widely used assay. The assay provides a rapid and sensitive method for detecting DNA-binding proteins based on the observation that the mobility of a DNA fragment through a nondenaturing, low-ionic strength polyacrylamide gel is retarded upon association with a DNA-binding protein (Fried and Crother, *Nucleic Acids Res.*

5   *9*:6505-6525 (1981), the entirety of which is herein incorporated by reference). When one or more specific binding activities have been identified, the exact sequence of the DNA bound by the protein may be determined. Several procedures for characterizing protein/DNA-binding sites are used, including methylation and ethylation interference assays (Maxam and Gilbert, *Methods Enzymol.* *65*:499-560 (1980), the entirety of which is herein incorporated by reference; Wissman

10   and Hillen, *Methods Enzymol.* *208*:365-379 (1991), the entirety of which is herein incorporated by reference), footprinting techniques employing DNase I (Galas and Schmitz, *Nucleic Acids Res.* *5*:3157-3170 (1978), the entirety of which is herein incorporated by reference), 1,10-phenanthroline-copper ion methods (Sigman *et al., Methods Enzymol.* *208*:414-433 (1991), the entirety of which is herein incorporated by reference) and hydroxyl radicals methods (Dixon *et*

15   *al., Methods Enzymol.* *208*:414-433 (1991), the entirety of which is herein incorporated by reference). It is understood that one or more of the nucleic acid molecules of the present invention may be utilized to identify a protein or fragment thereof that specifically binds to a nucleic acid molecule of the present invention. It is also understood that one or more of the protein molecules or fragments thereof of the present invention may be utilized to identify a

20   nucleic acid molecule that specifically binds to it.

A two-hybrid system is based on the fact that many cellular functions are carried out by proteins, such as transcription factors, that interact (physically) with one another. Two-hybrid systems have been used to probe the function of new proteins (Chien *et al., Proc. Natl. Acad. Sci.*

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(U.S.A.) 88:9578-9582 (1991) the entirety of which is herein incorporated by reference; Durfee *et al., Genes Dev. 7*:555-569 (1993) the entirety of which is herein incorporated by reference; Choi *et al., Cell 78*:499-512 (1994), the entirety of which is herein incorporated by reference; Kranz *et al., Genes Dev. 8*:313-327 (1994), the entirety of which is herein incorporated by reference).

5   Interaction mating techniques have facilitated a number of two-hybrid studies of protein-protein interaction. Interaction mating has been used to examine interactions between small sets of tens of proteins (Finley and Brent, *Proc. Natl. Acad. Sci. (U.S.A.) 91*:12098-12984 (1994), the entirety of which is herein incorporated by reference), larger sets of hundreds of proteins (Bendixen *et al., Nucl. Acids Res. 22*:1778-1779 (1994), the entirety of which is herein

10   incorporated by reference) and to comprehensively map proteins encoded by a small genome (Bartel *et al., Nature Genetics 12*:72-77 (1996), the entirety of which is herein incorporated by reference). This technique utilizes proteins fused to the DNA-binding domain and proteins fused to the activation domain. They are expressed in two different haploid yeast strains of opposite mating type and the strains are mated to determine if the two proteins interact. Mating occurs

15   when haploid yeast strains come into contact and result in the fusion of the two haploids into a diploid yeast strain. An interaction can be determined by the activation of a two-hybrid reporter gene in the diploid strain. An advantage of this technique is that it reduces the number of yeast transformations needed to test individual interactions. It is understood that the protein-protein interactions of protein or fragments thereof of the present invention may be investigated using

20   the two-hybrid system and that any of the nucleic acid molecules of the present invention that encode such proteins or fragments thereof may be used to transform yeast in the two-hybrid system.

(a)   **Plant Constructs and Plant Transformants**

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One or more of the nucleic acid molecules of the present invention may be used in plant transformation or transfection. Exogenous genetic material may be transferred into a plant cell and the plant cell regenerated into a whole, fertile or sterile plant. Exogenous genetic material is any genetic material, whether naturally occurring or otherwise, from any source that is capable of

5   being inserted into any organism. Such genetic material may be transferred into either monocotyledons and dicotyledons including, but not limited to maize (pp 63-69), soybean (pp 50-60), *Arabidopsis* (p 45), phaseolus (pp 47-49), peanut (pp 49-50), alfalfa (p 60), wheat (pp 69-71), rice (pp 72-79), oat (pp 80-81), sorghum (p 83), rye (p 84), tritordeum (p 84), millet (p85), fescue (p 85), perennial ryegrass (p 86), sugarcane (p87), cranberry (p101), papaya (pp 101-102),

10   banana (p 103), banana (p 103), muskmelon (p 104), apple (p 104), cucumber (p 105), dendrobium (p 109), gladiolus (p 110), chrysanthemum (p 110), liliacea (p 111), cotton (pp113-114), eucalyptus (p 115), sunflower (p 118), canola (p 118), turfgrass (p121), sugarbeet (p 122), coffee (p 122) and dioscorea (p 122) (Christou, In: *Particle Bombardment for Genetic Engineering of Plants*, Biotechnology Intelligence Unit. Academic Press, San Diego, California

15   (1996), the entirety of which is herein incorporated by reference).

Transfer of a nucleic acid that encodes for a protein can result in overexpression of that protein in a transformed cell or transgenic plant. One or more of the proteins or fragments thereof encoded by nucleic acid molecules of the present invention may be overexpressed in a transformed cell or transformed plant. Particularly, any of the phosphogluconate pathway

20   enzymes or fragments thereof may be overexpressed in a transformed cell or transgenic plant. Such overexpression may be the result of transient or stable transfer of the exogenous genetic material.

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Exogenous genetic material may be transferred into a plant cell and the plant cell by the use of a DNA vector or construct designed for such a purpose. Design of such a vector is generally within the skill of the art (*See, Plant Molecular Biology: A Laboratory Manual*, Clark (ed.), Springier, New York (1997), the entirety of which is herein incorporated by reference).

5   A construct or vector may include a plant promoter to express the protein or protein fragment of choice. A number of promoters which are active in plant cells have been described in the literature. These include the nopaline synthase (NOS) promoter (Ebert *et al., Proc. Natl. Acad. Sci. (U.S.A.) 84*:5745-5749 (1987), the entirety of which is herein incorporated by reference), the octopine synthase (OCS) promoter (which are carried on tumor-inducing plasmids of *Agrobacterium tumefaciens*), the caulimovirus promoters such as the cauliflower mosaic virus (CaMV) 19S promoter (Lawton *et al., Plant Mol. Biol. 9*:315-324 (1987), the entirety of which is herein incorporated by reference) and the CAMV 35S promoter (Odell *et al., Nature 313*:810-812 (1985), the entirety of which is herein incorporated by reference), the figwort mosaic virus 35S-promoter, the light-inducible promoter from the small subunit of ribulose-1,5-bis-phosphate carboxylase (ssRUBISCO), the Adh promoter (Walker *et al., Proc. Natl. Acad. Sci. (U.S.A.) 84*:6624-6628 (1987), the entirety of which is herein incorporated by reference), the sucrose synthase promoter (Yang *et al., Proc. Natl. Acad. Sci. (U.S.A.) 87*:4144-4148 (1990), the entirety of which is herein incorporated by reference), the R gene complex promoter (Chandler *et al., The Plant Cell 1*:1175-1183 (1989), the entirety of which is herein incorporated by reference) and the

20   chlorophyll a/b binding protein gene promoter, etc. These promoters have been used to create DNA constructs which have been expressed in plants; *see, e.g.,* PCT publication WO 84/02913, herein incorporated by reference in its entirety.

Promoters which are known or are found to cause transcription of DNA in plant cells can be used in the present invention. Such promoters may be obtained from a variety of sources such as plants and plant viruses. It is preferred that the particular promoter selected should be capable of causing sufficient expression to result in the production of an effective amount of the

5   phosphogluconate pathway enzyme to cause the desired phenotype. In addition to promoters that are known to cause transcription of DNA in plant cells, other promoters may be identified for use in the current invention by screening a plant cDNA library for genes which are selectively or preferably expressed in the target tissues or cells.

For the purpose of expression in source tissues of the plant, such as the leaf, seed, root or

10   stem, it is preferred that the promoters utilized in the present invention have relatively high expression in these specific tissues. For this purpose, one may choose from a number of promoters for genes with tissue- or cell-specific or -enhanced expression. Examples of such promoters reported in the literature include the chloroplast glutamine synthetase GS2 promoter from pea (Edwards *et al.*, *Proc. Natl. Acad. Sci. (U.S.A.) 87*:3459-3463 (1990), herein

15   incorporated by reference in its entirety), the chloroplast fructose-1,6-biphosphatase (FBPase) promoter from wheat (Lloyd *et al.*, *Mol. Gen. Genet. 225*:209-216 (1991), herein incorporated by reference in its entirety), the nuclear photosynthetic ST-LS1 promoter from potato (Stockhaus *et al.*, *EMBO J. 8*:2445-2451 (1989), herein incorporated by reference in its entirety), the serine/threonine kinase (PAL) promoter and the glucoamylase (CHS) promoter from *Arabidopsis*

20   *thaliana*. Also reported to be active in photosynthetically active tissues are the ribulose-1,5-bisphosphate carboxylase (RbcS) promoter from eastern larch (*Larix laricina*), the promoter for the *cab* gene, cab6, from pine (Yamamoto *et al.*, *Plant Cell Physiol. 35*:773-778 (1994), herein incorporated by reference in its entirety), the promoter for the Cab-1 gene from wheat (Fejes *et*

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al., Plant Mol. Biol. 15:921-932 (1990), herein incorporated by reference in its entirety), the

promoter for the CAB-1 gene from spinach (Lubberstedt *et al., Plant Physiol. 104*:997-1006

(1994), herein incorporated by reference in its entirety), the promoter for the cab1R gene from

rice (Luan *et al., Plant Cell. 4*:971-981 (1992), the entirety of which is herein incorporated by

5   reference), the pyruvate, orthophosphate dikinase (PPDK) promoter from maize (Matsuoka *et al.,*

Proc. Natl. Acad. Sci. (U.S.A.) 90: 9586-9590 (1993), herein incorporated by reference in its

entirety), the promoter for the tobacco Lhcb1*2 gene (Cerdan *et al., Plant Mol. Biol. 33*:245-255

(1997), herein incorporated by reference in its entirety), the *Arabidopsis thaliana* SUC2 sucrose-

H+ symporter promoter (Truernit *et al., Planta. 196*:564-570 (1995), herein incorporated by

10   reference in its entirety) and the promoter for the thylakoid membrane proteins from spinach

(psaD, psaF, psaE, PC, FNR, atpC, atpD, cab, rbcS). Other promoters for the chlorophyll a/b-

binding proteins may also be utilized in the present invention, such as the promoters for LhcB

gene and PsbP gene from white mustard (*Sinapis alba*; Kretsch *et al., Plant Mol. Biol. 28*:219-

229 (1995), the entirety of which is herein incorporated by reference).

15   For the purpose of expression in sink tissues of the plant, such as the tuber of the potato

plant, the fruit of tomato, or the seed of maize, wheat, rice and barley, it is preferred that the

promoters utilized in the present invention have relatively high expression in these specific

tissues. A number of promoters for genes with tuber-specific or -enhanced expression are

known, including the class I patatin promoter (Bevan *et al., EMBO J. 8*:1899-1906 (1986);

20   Jefferson *et al., Plant Mol. Biol. 14*:995-1006 (1990), both of which are herein incorporated by

reference in its entirety), the promoter for the potato tuber ADPGPP genes, both the large and

small subunits, the sucrose synthase promoter (Salanoubat and Belliard, *Gene. 60*:47-56 (1987),

Salanoubat and Belliard, *Gene. 84*:181-185 (1989), both of which are incorporated by reference

in their entirety), the promoter for the major tuber proteins including the 22 kd protein complexes and proteinase inhibitors (Hannapel, *Plant Physiol. 101*:703-704 (1993), herein incorporated by reference in its entirety), the promoter for the granule bound starch synthase gene (GBSS) (Visser *et al.*, *Plant Mol. Biol. 17*:691-699 (1991), herein incorporated by reference in its entirety) and other class I and II patatins promoters (Koster-Topfer *et al.*, *Mol Gen Genet. 219*:390-396 (1989); Mignery *et al.*, *Gene. 62*:27-44 (1988), both of which are herein incorporated by reference in their entirety).

Other promoters can also be used to express a phosphogluconate pathway enzyme or fragment thereof in specific tissues, such as seeds or fruits. The promoter for β-conglycinin (Chen *et al.*, *Dev. Genet. 10*: 112-122 (1989), herein incorporated by reference in its entirety) or other seed-specific promoters such as the napin and phaseolin promoters, can be used. The zeins are a group of storage proteins found in maize endosperm. Genomic clones for zein genes have been isolated (Pedersen *et al.*, *Cell 29*:1015-1026 (1982), herein incorporated by reference in its entirety) and the promoters from these clones, including the 15 kD, 16 kD, 19 kD, 22 kD, 27 kD and γ genes, could also be used. Other promoters known to function, for example, in maize include the promoters for the following genes: *waxy, Brittle, Shrunken 2*, Branching enzymes I and II, starch synthases, debranching enzymes, oleosins, glutelins and sucrose synthases. A particularly preferred promoter for maize endosperm expression is the promoter for the glutelin gene from rice, more particularly the Osgt-1 promoter (Zheng *et al.*, *Mol. Cell Biol. 13*:5829-5842 (1993), herein incorporated by reference in its entirety). Examples of promoters suitable for expression in wheat include those promoters for the ADPglucose pyrosynthase (ADPGPP) subunits, the granule bound and other starch synthase, the branching and debranching enzymes,

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the embryogenesis-abundant proteins, the gliadins and the glutenins. Examples of such promoters in rice include those promoters for the ADPGPP subunits, the granule bound and other starch synthase, the branching enzymes, the debranching enzymes, sucrose synthases and the glutelins. A particularly preferred promoter is the promoter for rice glutelin, Osgt-1. Examples of such promoters for barley include those for the ADPGPP subunits, the granule bound and other starch synthase, the branching enzymes, the debranching enzymes, sucrose synthases, the hordeins, the embryo globulins and the aleurone specific proteins.

Root specific promoters may also be used. An example of such a promoter is the promoter for the acid chitinase gene (Samac *et al.*, *Plant Mol. Biol. 25*:587-596 (1994), the entirety of which is herein incorporated by reference). Expression in root tissue could also be accomplished by utilizing the root specific subdomains of the CaMV35S promoter that have been identified (Lam *et al.*, *Proc. Natl. Acad. Sci. (U.S.A.) 86*:7890-7894 (1989), herein incorporated by reference in its entirety). Other root cell specific promoters include those reported by Conkling *et al.* (Conkling *et al.*, *Plant Physiol. 93*:1203-1211 (1990), the entirety of which is herein incorporated by reference).

Additional promoters that may be utilized are described, for example, in U.S. Patent Nos. 5,378,619; 5,391,725; 5,428,147; 5,447,858; 5,608,144; 5,608,144; 5,614,399; 5,633,441; 5,633,435; and 4,633,436, all of which are herein incorporated in their entirety. In addition, a tissue specific enhancer may be used (Fromm *et al.*, *The Plant Cell 1*:977-984 (1989), the entirety of which is herein incorporated by reference).

Constructs or vectors may also include with the coding region of interest a nucleic acid sequence that acts, in whole or in part, to terminate transcription of that region. For example, such sequences have been isolated including the Tr7 3' sequence and the NOS 3' sequence

(Ingelbrecht *et al.*, *The Plant Cell 1*:671-680 (1989), the entirety of which is herein incorporated by reference; Bevan *et al.*, *Nucleic Acids Res. 11*:369-385 (1983), the entirety of which is herein incorporated by reference), or the like.

A vector or construct may also include regulatory elements. Examples of such include the Adh intron 1 (Callis *et al.*, *Genes and Develop. 1*:1183-1200 (1987), the entirety of which is herein incorporated by reference), the sucrose synthase intron (Vasil *et al.*, Plant Physiol. 91:1575-1579 (1989), the entirety of which is herein incorporated by reference) and the TMV omega element (Gallie *et al.*, *The Plant Cell 1*:301-311 (1989), the entirety of which is herein incorporated by reference). These and other regulatory elements may be included when appropriate.

A vector or construct may also include a selectable marker. Selectable markers may also be used to select for plants or plant cells that contain the exogenous genetic material. Examples of such include, but are not limited to, a neo gene (Potrykus *et al.*, *Mol. Gen. Genet. 199*:183-188 (1985), the entirety of which is herein incorporated by reference) which codes for kanamycin resistance and can be selected for using kanamycin, G418, etc.; a bar gene which codes for bialaphos resistance; a mutant EPSP synthase gene (Hinchee *et al.*, *Bio/Technology 6*:915-922 (1988), the entirety of which is herein incorporated by reference) which encodes glyphosate resistance; a nitrilase gene which confers resistance to bromoxynil (Stalker *et al.*, *J. Biol. Chem. 263*:6310-6314 (1988), the entirety of which is herein incorporated by reference); a mutant acetolactate synthase gene (ALS) which confers imidazolinone or sulphonylurea resistance (European Patent Application 154,204 (Sept. 11, 1985), the entirety of which is herein incorporated by reference); and a methotrexate resistant DHFR gene (Thillet *et al.*, *J. Biol. Chem. 263*:12500-12508 (1988), the entirety of which is herein incorporated by reference).

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A vector or construct may also include a transit peptide. Incorporation of a suitable chloroplast transit peptide may also be employed (European Patent Application Publication Number 0218571, the entirety of which is herein incorporated by reference). Translational enhancers may also be incorporated as part of the vector DNA. DNA constructs could contain

5   one or more 5' non-translated leader sequences which may serve to enhance expression of the gene products from the resulting mRNA transcripts. Such sequences may be derived from the promoter selected to express the gene or can be specifically modified to increase translation of the mRNA. Such regions may also be obtained from viral RNAs, from suitable eukaryotic genes, or from a synthetic gene sequence. For a review of optimizing expression of transgenes,

10 see Koziel et al., Plant Mol. Biol. 32:393-405 (1996), the entirety of which is herein incorporated by reference.

A vector or construct may also include a screenable marker. Screenable markers may be used to monitor expression. Exemplary screenable markers include a β-glucuronidase or uidA gene (GUS) which encodes an enzyme for which various chromogenic substrates are known

15 (Jefferson, Plant Mol. Biol, Rep. 5:387-405 (1987), the entirety of which is herein incorporated by reference; Jefferson et al., EMBO J. 6:3901-3907 (1987), the entirety of which is herein incorporated by reference); an R-locus gene, which encodes a product that regulates the production of anthocyanin pigments (red color) in plant tissues (Dellaporta et al., Stadler Symposium 11:263-282 (1988), the entirety of which is herein incorporated by reference); a β-

20 lactamase gene (Sutcliffe et al., Proc. Natl. Acad. Sci. (U.S.A.) 75:3737-3741 (1978), the entirety of which is herein incorporated by reference), a gene which encodes an enzyme for which various chromogenic substrates are known (e.g., PADAC, a chromogenic cephalosporin); a

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luciferase gene (Ow *et al.*, *Science 234*:856-859 (1986), the entirety of which is herein

incorporated by reference); a xylE gene (Zukowsky *et al.*, *Proc. Natl. Acad. Sci. (U.S.A.)*

80:1101-1105 (1983), the entirety of which is herein incorporated by reference) which encodes a

catechol diozygenase that can convert chromogenic catechols; an α-amylase gene (Ikatu *et al.*,

5   *Bio/Technol. 8*:241-242 (1990), the entirety of which is herein incorporated by reference); a

tyrosinase gene (Katz *et al.*, *J. Gen. Microbiol. 129*:2703-2714 (1983), the entirety of which is

herein incorporated by reference) which encodes an enzyme capable of oxidizing tyrosine to

DOPA and dopaquinone which in turn condenses to melanin; an α-galactosidase, which will turn

a chromogenic α-galactose substrate.

10   Included within the terms "selectable or screenable marker genes" are also genes which

encode a secretable marker whose secretion can be detected as a means of identifying or

selecting for transformed cells. Examples include markers which encode a secretable antigen

that can be identified by antibody interaction, or even secretable enzymes which can be detected

catalytically. Secretable proteins fall into a number of classes, including small, diffusible

15   proteins which are detectable, (*e.g.*, by ELISA), small active enzymes which are detectable in

extracellular solution (*e.g.*, α-amylase, β-lactamase, phosphinothricin transferase), or proteins

which are inserted or trapped in the cell wall (such as proteins which include a leader sequence

such as that found in the expression unit of extension or tobacco PR-S). Other possible

selectable and/or screenable marker genes will be apparent to those of skill in the art.

20   There are many methods for introducing transforming nucleic acid molecules into plant

cells. Suitable methods are believed to include virtually any method by which nucleic acid

molecules may be introduced into a cell, such as by *Agrobacterium* infection or direct delivery of

nucleic acid molecules such as, for example, by PEG-mediated transformation, by electroporation or by acceleration of DNA coated particles, etc (Potrykus, *Ann. Rev. Plant Physiol. Plant Mol. Biol. 42*:205-225 (1991), the entirety of which is herein incorporated by reference; Vasil, *Plant Mol. Biol. 25*:925-937 (1994), the entirety of which is herein incorporated by reference). For example, electroporation has been used to transform maize protoplasts (Fromm *et al., Nature 312*:791-793 (1986), the entirety of which is herein incorporated by reference).

Other vector systems suitable for introducing transforming DNA into a host plant cell include but are not limited to binary artificial chromosome (BIBAC) vectors (Hamilton *et al., Gene 200*:107-116 (1997), the entirety of which is herein incorporated by reference); and transfection with RNA viral vectors (Della-Cioppa *et al., Ann. N.Y. Acad. Sci.* (1996), 792 (Engineering Plants for Commercial Products and Applications), 57-61, the entirety of which is herein incorporated by reference). Additional vector systems also include plant selectable YAC vectors such as those described in Mullen *et al., Molecular Breeding 4*:449-457 (1988), the entireity of which is herein incorporated by reference).

Technology for introduction of DNA into cells is well known to those of skill in the art. Four general methods for delivering a gene into cells have been described: (1) chemical methods (Graham and van der Eb, *Virology 54*:536-539 (1973), the entirety of which is herein incorporated by reference); (2) physical methods such as microinjection (Capecchi, *Cell 22*:479-488 (1980), the entirety of which is herein incorporated by reference), electroporation (Wong and Neumann, *Biochem. Biophys. Res. Commun. 107*:584-587 (1982); Fromm *et al., Proc. Natl. Acad. Sci. (U.S.A.) 82*:5824-5828 (1985); U.S. Patent No. 5,384,253, all of which are herein incorporated in their entirety); and the gene gun (Johnston and Tang, *Methods Cell Biol. 43*:353-

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365 (1994), the entirety of which is herein incorporated by reference); (3) viral vectors (Clapp, *Clin. Perinatol.* *20*:155-168 (1993); Lu *et al.*, *J. Exp. Med.* *178*:2089-2096 (1993); Eglitis and Anderson, *Biotechniques* *6*:608-614 (1988), all of which are herein incorporated in their entirety); and (4) receptor-mediated mechanisms (Curiel *et al.*, *Hum. Gen. Ther.* *3*:147-154 (1992), Wagner *et al.*, *Proc. Natl. Acad. Sci. (USA)* *89*:6099-6103 (1992), both of which are incorporated by reference in their entirety).

Acceleration methods that may be used include, for example, microprojectile bombardment and the like. One example of a method for delivering transforming nucleic acid molecules to plant cells is microprojectile bombardment. This method has been reviewed by Yang and Christou (eds.), *Particle Bombardment Technology for Gene Transfer*, Oxford Press, Oxford, England (1994), the entirety of which is herein incorporated by reference). Non-biological particles (microprojectiles) that may be coated with nucleic acids and delivered into cells by a propelling force. Exemplary particles include those comprised of tungsten, gold, platinum and the like.

A particular advantage of microprojectile bombardment, in addition to it being an effective means of reproducibly transforming monocots, is that neither the isolation of protoplasts (Cristou *et al.*, *Plant Physiol.* *87*:671-674 (1988), the entirety of which is herein incorporated by reference) nor the susceptibility of *Agrobacterium* infection are required. An illustrative embodiment of a method for delivering DNA into maize cells by acceleration is a biolistics α-particle delivery system, which can be used to propel particles coated with DNA through a screen, such as a stainless steel or Nytex screen, onto a filter surface covered with corn cells cultured in suspension. Gordon-Kamm *et al.*, describes the basic procedure for coating

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tungsten particles with DNA (Gordon-Kamm *et al.*, *Plant Cell 2*:603-618 (1990), the entirety of which is herein incorporated by reference). The screen disperses the tungsten nucleic acid particles so that they are not delivered to the recipient cells in large aggregates. A particle delivery system suitable for use with the present invention is the helium acceleration PDS-

5   1000/He gun is available from Bio-Rad Laboratories (Bio-Rad, Hercules, California)(Sanford *et al.*, *Technique 3*:3-16 (1991), the entirety of which is herein incorporated by reference).

For the bombardment, cells in suspension may be concentrated on filters. Filters containing the cells to be bombarded are positioned at an appropriate distance below the microprojectile stopping plate. If desired, one or more screens are also positioned between the

10   gun and the cells to be bombarded.

Alternatively, immature embryos or other target cells may be arranged on solid culture medium. The cells to be bombarded are positioned at an appropriate distance below the microprojectile stopping plate. If desired, one or more screens are also positioned between the acceleration device and the cells to be bombarded. Through the use of techniques set forth herein

15   one may obtain up to 1000 or more foci of cells transiently expressing a marker gene. The number of cells in a focus which express the exogenous gene product 48 hours post-bombardment often range from one to ten and average one to three.

In bombardment transformation, one may optimize the pre-bombardment culturing conditions and the bombardment parameters to yield the maximum numbers of stable

20   transformants. Both the physical and biological parameters for bombardment are important in this technology. Physical factors are those that involve manipulating the DNA/microprojectile precipitate or those that affect the flight and velocity of either the macro- or microprojectiles. Biological factors include all steps involved in manipulation of cells before and immediately

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after bombardment, the osmotic adjustment of target cells to help alleviate the trauma associated with bombardment and also the nature of the transforming DNA, such as linearized DNA or intact supercoiled plasmids. It is believed that pre-bombardment manipulations are especially important for successful transformation of immature embryos.

5   In another alternative embodiment, plastids can be stably transformed. Methods disclosed for plastid transformation in higher plants include the particle gun delivery of DNA containing a selectable marker and targeting of the DNA to the plastid genome through homologous recombination (Svab *et al., Proc. Natl. Acad. Sci. (U.S.A.) 87*:8526-8530 (1990); Svab and Maliga, *Proc. Natl. Acad. Sci. (U.S.A.) 90*:913-917 (1993); Staub and Maliga, *EMBO J. 12*:601-606 (1993); U.S. Patent Nos. 5, 451,513 and 5,545,818, all of which are herein incorporated by reference in their entirety).

    Accordingly, it is contemplated that one may wish to adjust various aspects of the bombardment parameters in small scale studies to fully optimize the conditions. One may particularly wish to adjust physical parameters such as gap distance, flight distance, tissue

15 distance and helium pressure. One may also minimize the trauma reduction factors by modifying conditions which influence the physiological state of the recipient cells and which may therefore influence transformation and integration efficiencies. For example, the osmotic state, tissue hydration and the subculture stage or cell cycle of the recipient cells may be adjusted for optimum transformation. The execution of other routine adjustments will be known to those of

20 skill in the art in light of the present disclosure.

    Agrobacterium-mediated transfer is a widely applicable system for introducing genes into plant cells because the DNA can be introduced into whole plant tissues, thereby bypassing the need for regeneration of an intact plant from a protoplast. The use of *Agrobacterium*-mediated

plant integrating vectors to introduce DNA into plant cells is well known in the art. See, for

example the methods described by Fraley *et al., Bio/Technology* 3:629-635 (1985) and Rogers *et

al., Methods Enzymol.* 153:253-277 (1987), both of which are herein incorporated by reference in

their entirety. Further, the integration of the Ti-DNA is a relatively precise process resulting in

5 few rearrangements. The region of DNA to be transferred is defined by the border sequences and

intervening DNA is usually inserted into the plant genome as described (Spielmann *et al., Mol.

Gen. Genet.* 205:34 (1986), the entirety of which is herein incorporated by reference).

Modern *Agrobacterium* transformation vectors are capable of replication in E. *coli* as

well as *Agrobacterium*, allowing for convenient manipulations as described (Klee *et al.,* In: *Plant

10 DNA Infectious Agents*, Hohn and Schell (eds.), Springer-Verlag, New York, pp. 179-203 (1985),

the entirety of which is herein incorporated by reference. Moreover, technological advances in

vectors for *Agrobacterium*-mediated gene transfer have improved the arrangement of genes and

restriction sites in the vectors to facilitate construction of vectors capable of expressing various

polypeptide coding genes. The vectors described have convenient multi-linker regions flanked

15 by a promoter and a polyadenylation site for direct expression of inserted polypeptide coding

genes and are suitable for present purposes (Rogers *et al., Methods Enzymol.* 153:253-277

(1987)). In addition, *Agrobacterium* containing both armed and disarmed Ti genes can be used

for the transformations. In those plant strains where *Agrobacterium*-mediated transformation is

efficient, it is the method of choice because of the facile and defined nature of the gene transfer.

20 A transgenic plant formed using *Agrobacterium* transformation methods typically

contains a single gene on one chromosome. Such transgenic plants can be referred to as being

heterozygous for the added gene. More preferred is a transgenic plant that is homozygous for the

added structural gene; *i.e.*, a transgenic plant that contains two added genes, one gene at the same

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locus on each chromosome of a chromosome pair. A homozygous transgenic plant can be obtained by sexually mating (selfing) an independent segregant transgenic plant that contains a single added gene, germinating some of the seed produced and analyzing the resulting plants produced for the gene of interest.

5   It is also to be understood that two different transgenic plants can also be mated to produce offspring that contain two independently segregating added, exogenous genes. Selfing of appropriate progeny can produce plants that are homozygous for both added, exogenous genes that encode a polypeptide of interest. Back-crossing to a parental plant and out-crossing with a non-transgenic plant are also contemplated, as is vegetative propagation.

10   Transformation of plant protoplasts can be achieved using methods based on calcium phosphate precipitation, polyethylene glycol treatment, electroporation and combinations of these treatments (*See, for example*, Potrykus *et al., Mol. Gen. Genet. 205*:193-200 (1986); Lorz *et al., Mol. Gen. Genet. 199*:178 (1985); Fromm *et al., Nature 319*:791 (1986); Uchimiya *et al., Mol. Gen. Genet. 204*:204 (1986); Marcotte *et al., Nature 335*:454-457 (1988), all of which are

15 herein incorporated by reference in their entirety).

       Application of these systems to different plant strains depends upon the ability to regenerate that particular plant strain from protoplasts. Illustrative methods for the regeneration of cereals from protoplasts are described (Fujimura *et al., Plant Tissue Culture Letters 2*:74 (1985); Toriyama *et al., Theor Appl. Genet. 205*:34 (1986); Yamada *et al., Plant Cell Rep. 4*:85

20 (1986); Abdullah *et al., Biotechnolog 4*:1087 (1986), all of which are herein incorporated by reference in their entirety).

       To transform plant strains that cannot be successfully regenerated from protoplasts, other ways to introduce DNA into intact cells or tissues can be utilized. For example, regeneration of

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cereals from immature embryos or explants can be effected as described (Vasil, *Biotechnology* *6*:397 (1988), the entirety of which is herein incorporated by reference). In addition, "particle gun" or high-velocity microprojectile technology can be utilized (Vasil *et al.*, *Bio/Technology* *10*:667 (1992), the entirety of which is herein incorporated by reference).

5   Using the latter technology, DNA is carried through the cell wall and into the cytoplasm on the surface of small metal particles as described (Klein *et al.*, *Nature 328:*70 (1987); Klein *et al.*, *Proc. Natl. Acad. Sci. (U.S.A.)* *85*:8502-8505 (1988); McCabe *et al.*, *Bio/Technology 6:923* (1988), all of which are herein incorporated by reference in their entirety). The metal particles penetrate through several layers of cells and thus allow the transformation of cells within tissue explants.

          Other methods of cell transformation can also be used and include but are not limited to introduction of DNA into plants by direct DNA transfer into pollen (Zhou *et al.*, *Methods Enzymol. 101:*433 (1983); Hess *et al.*, *Intern Rev. Cytol. 107:*367 (1987); Luo *et al.*, *Plant Mol Biol. Reporter 6:*165 (1988), all of which are herein incorporated by reference in their entirety), by direct injection of DNA into reproductive organs of a plant (Pena *et al.*, *Nature 325*:274 (1987), the entirety of which is herein incorporated by reference), or by direct injection of DNA into the cells of immature embryos followed by the rehydration of desiccated embryos (Neuhaus *et al.*, *Theor. Appl. Genet. 75*:30 (1987), the entirety of which is herein incorporated by reference).

20   The regeneration, development and cultivation of plants from single plant protoplast transformants or from various transformed explants is well known in the art (Weissbach and Weissbach, In: *Methods for Plant Molecular Biology*, Academic Press, San Diego, CA, (1988), the entirety of which is herein incorporated by reference). This regeneration and growth process

typically includes the steps of selection of transformed cells, culturing those individualized cells through the usual stages of embryonic development through the rooted plantlet stage. Transgenic embryos and seeds are similarly regenerated. The resulting transgenic rooted shoots are thereafter planted in an appropriate plant growth medium such as soil.

5   The development or regeneration of plants containing the foreign, exogenous gene that encodes a protein of interest is well known in the art. Preferably, the regenerated plants are self-pollinated to provide homozygous transgenic plants. Otherwise, pollen obtained from the regenerated plants is crossed to seed-grown plants of agronomically important lines. Conversely, pollen from plants of these important lines is used to pollinate regenerated plants. A transgenic

10   plant of the present invention containing a desired polypeptide is cultivated using methods well known to one skilled in the art.

There are a variety of methods for the regeneration of plants from plant tissue. The particular method of regeneration will depend on the starting plant tissue and the particular plant species to be regenerated.

15   Methods for transforming dicots, primarily by use of *Agrobacterium tumefaciens* and obtaining transgenic plants have been published for cotton (U.S. Patent No. 5,004,863; U.S. Patent No. 5,159,135; U.S. Patent No. 5,518,908, all of which are herein incorporated by reference in their entirety); soybean (U.S. Patent No. 5,569,834; U.S. Patent No. 5,416,011; McCabe *et. al., Biotechnology 6:*923 (1988); Christou *et al., Plant Physiol. 87:*671-674 (1988);

20   all of which are herein incorporated by reference in their entirety); *Brassica* (U.S. Patent No. 5,463,174, the entirety of which is herein incorporated by reference); peanut (Cheng *et al., Plant Cell Rep. 15:*653-657 (1996), McKently *et al., Plant Cell Rep. 14:*699-703 (1995), all of which

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are herein incorporated by reference in their entirety); papaya; and pea (Grant *et al., Plant Cell Rep. 15*:254-258 (1995), the entirety of which is herein incorporated by reference).

Transformation of monocotyledons using electroporation, particle bombardment and *Agrobacterium* have also been reported. Transformation and plant regeneration have been achieved in asparagus (Bytebier *et al., Proc. Natl. Acad. Sci. (USA) 84*:5354 (1987), the entirety of which is herein incorporated by reference); barley (Wan and Lemaux, *Plant Physiol 104*:37 (1994), the entirety of which is herein incorporated by reference); maize (Rhodes *et al., Science 240*:204 (1988); Gordon-Kamm *et al., Plant Cell 2*:603-618 (1990); Fromm *et al., Bio/Technology 8*:833 (1990); Koziel *et al., Bio/Technology 11*:194 (1993); Armstrong *et al., Crop Science 35*:550-557 (1995); all of which are herein incorporated by reference in their entirety); oat (Somers *et al., Bio/Technology 10*:1589 (1992), the entirety of which is herein incorporated by reference); orchard grass (Horn *et al., Plant Cell Rep. 7*:469 (1988), the entirety of which is herein incorporated by reference); rice (Toriyama *et al., Theor Appl. Genet. 205*:34 (1986); Part *et al., Plant Mol. Biol. 32*:1135-1148 (1996); Abedinia *et al., Aust. J. Plant Physiol. 24*:133-141 (1997); Zhang and Wu, *Theor. Appl. Genet. 76*:835 (1988); Zhang *et al., Plant Cell Rep. 7*:379 (1988); Battraw and Hall, *Plant Sci. 86*:191-202 (1992); Christou *et al., Bio/Technology 9*:957 (1991), all of which are herein incorporated by reference in their entirety); rye (De la Pena *et al., Nature 325*:274 (1987), the entirety of which is herein incorporated by reference); sugarcane (Bower and Birch, *Plant J. 2*:409 (1992), the entirety of which is herein incorporated by reference); tall fescue (Wang *et al., Bio/Technology 10*:691 (1992), the entirety of which is herein incorporated by reference) and wheat (Vasil *et al., Bio/Technology 10*:667 (1992), the entirety of which is herein incorporated by reference; U.S. Patent No. 5,631,152, the entirety of which is herein incorporated by reference.)

Assays for gene expression based on the transient expression of cloned nucleic acid constructs have been developed by introducing the nucleic acid molecules into plant cells by polyethylene glycol treatment, electroporation, or particle bombardment (Marcotte *et al., Nature 335*:454-457 (1988), the entirety of which is herein incorporated by reference; Marcotte *et al.,*

5   *Plant Cell 1*:523-532 (1989), the entirety of which is herein incorporated by reference; McCarty *et al., Cell 66*:895-905 (1991), the entirety of which is herein incorporated by reference; Hattori *et al., Genes Dev. 6*:609-618 (1992), the entirety of which is herein incorporated by reference; Goff *et al., EMBO J. 9*:2517-2522 (1990), the entirety of which is herein incorporated by reference). Transient expression systems may be used to functionally dissect gene constructs

10   (*see generally*, Mailga *et al., Methods in Plant Molecular Biology,* Cold Spring Harbor Press (1995)).

Any of the nucleic acid molecules of the present invention may be introduced into a plant cell in a permanent or transient manner in combination with other genetic elements such as vectors, promoters, enhancers etc. Further, any of the nucleic acid molecules of the present

15   invention may be introduced into a plant cell in a manner that allows for overexpression of the protein or fragment thereof encoded by the nucleic acid molecule.

Cosuppression is the reduction in expression levels, usually at the level of RNA, of a particular endogenous gene or gene family by the expression of a homologous sense construct that is capable of transcribing mRNA of the same strandedness as the transcript of the

20   endogenous gene (Napoli *et al., Plant Cell 2*:279-289 (1990), the entirety of which is herein incorporated by reference; van der Krol *et al., Plant Cell 2*:291-299 (1990), the entirety of which is herein incorporated by reference). Cosuppression may result from stable transformation with a single copy nucleic acid molecule that is homologous to a nucleic acid sequence found with the

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cell (Prolls and Meyer, *Plant J. 2*:465-475 (1992), the entirety of which is herein incorporated by reference) or with multiple copies of a nucleic acid molecule that is homologous to a nucleic acid sequence found with the cell (Mittlesten *et al., Mol. Gen. Genet. 244*:325-330 (1994), the entirety of which is herein incorporated by reference). Genes, even though different, linked to

5   homologous promoters may result in the cosuppression of the linked genes (Vaucheret, *C.R. Acad. Sci. III 316*:1471-1483 (1993), the entirety of which is herein incorporated by reference).

This technique has, for example, been applied to generate white flowers from red petunia and tomatoes that do not ripen on the vine. Up to 50% of petunia transformants that contained a sense copy of the glucoamylase (CHS) gene produced white flowers or floral sectors; this was as

10   a result of the post-transcriptional loss of mRNA encoding CHS (Flavell, *Proc. Natl. Acad. Sci. (U.S.A.) 91*:3490-3496 (1994), the entirety of which is herein incorporated by reference); van Blokland *et al., Plant J. 6*:861-877 (1994), the entirety of which is herein incorporated by reference). Cosuppression may require the coordinate transcription of the transgene and the endogenous gene and can be reset by a developmental control mechanism (Jorgensen, *Trends*

15   *Biotechnol. 8*:340-344 (1990), the entirety of which is herein incorporated by reference; Meins and Kunz, In: *Gene Inactivation and Homologous Recombination in Plants*, Paszkowski (ed.), pp. 335-348, Kluwer Academic, Netherlands (1994), the entirety of which is herein incorporated by reference).

It is understood that one or more of the nucleic acids of the present invention may be

20   introduced into a plant cell and transcribed using an appropriate promoter with such transcription resulting in the cosuppression of an endogenous phosphogluconate pathway enzyme.

Antisense approaches are a way of preventing or reducing gene function by targeting the genetic material (Mol *et al., FEBS Lett. 268*:427-430 (1990), the entirety of which is herein

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incorporated by reference). The objective of the antisense approach is to use a sequence complementary to the target gene to block its expression and create a mutant cell line or organism in which the level of a single chosen protein is selectively reduced or abolished. Antisense techniques have several advantages over other 'reverse genetic' approaches. The site

5   of inactivation and its developmental effect can be manipulated by the choice of promoter for antisense genes or by the timing of external application or microinjection. Antisense can manipulate its specificity by selecting either unique regions of the target gene or regions where it shares homology to other related genes (Hiatt *et al.*, In: *Genetic Engineering*, Setlow (ed.), Vol. 11, New York: Plenum 49-63 (1989), the entirety of which is herein incorporated by reference).

10   The principle of regulation by antisense RNA is that RNA that is complementary to the target mRNA is introduced into cells, resulting in specific RNA:RNA duplexes being formed by base pairing between the antisense substrate and the target mRNA (Green *et al.*, *Annu. Rev. Biochem.* 55:569-597 (1986), the entirety of which is herein incorporated by reference). Under one embodiment, the process involves the introduction and expression of an antisense gene

15   sequence. Such a sequence is one in which part or all of the normal gene sequences are placed under a promoter in inverted orientation so that the 'wrong' or complementary strand is transcribed into a noncoding antisense RNA that hybridizes with the target mRNA and interferes with its expression (Takayama and Inouye, *Crit. Rev. Biochem. Mol. Biol.* 25:155-184 (1990), the entirety of which is herein incorporated by reference). An antisense vector is constructed by

20   standard procedures and introduced into cells by transformation, transfection, electroporation, microinjection, infection, etc. The type of transformation and choice of vector will determine whether expression is transient or stable. The promoter used for the antisense gene may influence the level, timing, tissue, specificity, or inducibility of the antisense inhibition.

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It is understood that the activity of a phosphogluconate pathway enzyme in a plant cell

may be reduced or depressed by growing a transformed plant cell containing a nucleic acid

molecule whose non-transcribed strand encodes a phosphogluconate pathway enzyme or

fragment thereof.

5   Antibodies have been expressed in plants (Hiatt *et al., Nature 342:*76-78 (1989), the

entirety of which is herein incorporated by reference; Conrad and Fielder, *Plant Mol. Biol.*

*26:*1023-1030 (1994), the entirety of which is herein incorporated by reference). Cytoplamsic

expression of a scFv (single-chain Fv antibodies) has been reported to delay infection by

artichoke mottled crinkle virus. Transgenic plants that express antibodies directed against

10   endogenous proteins may exhibit a physiological effect (Philips *et al., EMBO J. 16:*4489-4496

(1997), the entirety of which is herein incorporated by reference; Marion-Poll, *Trends in Plant*

*Science 2:*447-448 (1997), the entirety of which is herein incorporated by reference). For

example, expressed anti-abscisic antibodies have been reported to result in a general perturbation

of seed development (Philips *et al., EMBO J. 16:* 4489-4496 (1997)).

15   Antibodies that are catalytic may also be expressed in plants (abzymes). The principle

behind abzymes is that since antibodies may be raised against many molecules, this recognition

ability can be directed toward generating antibodies that bind transition states to force a chemical

reaction forward (Persidas, *Nature Biotechnology 15:*1313-1315 (1997), the entirety of which is

herein incorporated by reference; Baca *et al., Ann. Rev. Biophys. Biomol. Struct. 26:*461-493

20   (1997), the entirety of which is herein incorporated by reference). The catalytic abilities of

abzymes may be enhanced by site directed mutagenesis. Examples of abzymes are, for example,

set forth in U.S. Patent No. 5,658,753; U.S. Patent No. 5,632,990; U.S. Patent No. 5,631,137;

U.S. Patent No. 5,602,015; U.S. Patent No. 5,559,538; U.S. Patent No. 5,576,174; U.S. Patent

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No. 5,500,358; U.S. Patent No. 5,318,897; U.S. Patent No. 5,298,409; U.S. Patent No. 5,258,289 and U.S. Patent No. 5,194,585, all of which are herein incorporated in their entirety.

It is understood that any of the antibodies of the present invention may be expressed in plants and that such expression can result in a physiological effect. It is also understood that any of the expressed antibodies may be catalytic.

(b)   Fungal Constructs and Fungal Transformants

The present invention also relates to a fungal recombinant vector comprising exogenous genetic material. The present invention also relates to a fungal cell comprising a fungal recombinant vector. The present invention also relates to methods for obtaining a recombinant fungal host cell comprising introducing into a fungal host cell exogenous genetic material.

Exogenous genetic material may be transferred into a fungal cell. In a preferred embodiment the exogenous genetic material includes a nucleic acid molecule of the present invention having a sequence selected from the group consisting of SEQ ID NO: 1 through SEQ ID NO: 699 or complements thereof or fragments of either or other nucleic acid molecule of the present invention. The fungal recombinant vector may be any vector which can be conveniently subjected to recombinant DNA procedures. The choice of a vector will typically depend on the compatibility of the vector with the fungal host cell into which the vector is to be introduced. The vector may be a linear or a closed circular plasmid. The vector system may be a single vector or plasmid or two or more vectors or plasmids which together contain the total DNA to be introduced into the genome of the fungal host.

The fungal vector may be an autonomously replicating vector, *i.e.,* a vector which exists as an extrachromosomal entity, the replication of which is independent of chromosomal replication, *e.g.,* a plasmid, an extrachromosomal element, a minichromosome, or an artificial

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chromosome. The vector may contain any means for assuring self-replication. Alternatively, the vector may be one which, when introduced into the fungal cell, is integrated into the genome and replicated together with the chromosome(s) into which it has been integrated. For integration, the vector may rely on the nucleic acid sequence of the vector for stable integration of the vector into the genome by homologous or nonhomologous recombination. Alternatively, the vector may contain additional nucleic acid sequences for directing integration by homologous recombination into the genome of the fungal host. The additional nucleic acid sequences enable the vector to be integrated into the host cell genome at a precise location(s) in the chromosome(s). To increase the likelihood of integration at a precise location, there should be preferably two nucleic acid sequences which individually contain a sufficient number of nucleic acids, preferably 400bp to 1500bp, more preferably 800bp to 1000bp, which are highly homologous with the corresponding target sequence to enhance the probability of homologous recombination. These nucleic acid sequences may be any sequence that is homologous with a target sequence in the genome of the fungal host cell and, furthermore, may be non-encoding or encoding sequences.

For autonomous replication, the vector may further comprise an origin of replication enabling the vector to replicate autonomously in the host cell in question. Examples of origin of replications for use in a yeast host cell are the 2 micron origin of replication and the combination of CEN3 and ARS 1. Any origin of replication may be used which is compatible with the fungal host cell of choice.

The fungal vectors of the present invention preferably contain one or more selectable markers which permit easy selection of transformed cells. A selectable marker is a gene the product of which provides, for example biocide or viral resistance, resistance to heavy metals,

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prototrophy to auxotrophs and the like. The selectable marker may be selected from the group

including, but not limited to, *amdS* (acetamidase), *argB* (ornithine carbamoyltransferase), *bar*

(phosphinothricin acetyltransferase), hygB (hygromycin phosphotransferase), *niaD* (nitrate

reductase), *pyrG* (orotidine-5'-phosphate decarboxylase) and *sC* (sulfate adenyltransferase) and

5   *trpC* (anthranilate synthase). Preferred for use in an *Aspergillus* cell are the *amdS* and *pyrG*

markers of *Aspergillus nidulans* or *Aspergillus oryzae* and the bar marker of *Streptomyces*

hygroscopicus. Furthermore, selection may be accomplished by co-transformation, *e.g.*, as

described in WO 91/17243, the entirety of which is herein incorporated by reference. A nucleic

acid sequence of the present invention may be operably linked to a suitable promoter sequence.

10   The promoter sequence is a nucleic acid sequence which is recognized by the fungal host cell for

expression of the nucleic acid sequence. The promoter sequence contains transcription and

translation control sequences which mediate the expression of the protein or fragment thereof.

A promoter may be any nucleic acid sequence which shows transcriptional activity in the

fungal host cell of choice and may be obtained from genes encoding polypeptides either

15   homologous or heterologous to the host cell. Examples of suitable promoters for directing the

transcription of a nucleic acid construct of the invention in a filamentous fungal host are

promoters obtained from the genes encoding *Aspergillus oryzae* TAKA amylase, *Rhizomucor*

miehei aspartic proteinase, *Aspergillus niger* neutral alpha-amylase, *Aspergillus niger* acid stable

alpha-amylase, *Aspergillus niger* or *Aspergillus awamori* glucoamylase (glaA), *Rhizomucor*

20   *miehei* lipase, *Aspergillus oryzae* alkaline protease, *Aspergillus oryzae* triose phosphate

isomerase, *Aspergillus nidulans* acetamidase and hybrids thereof. In a yeast host, a useful

promoter is the *Saccharomyces cerevisiae* enolase (eno-1) promoter. Particularly preferred

promoters are the TAKA amylase, NA2-tpi (a hybrid of the promoters from the genes encoding

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Aspergillus niger neutral alpha -amylase and *Aspergillus oryzae* triose phosphate isomerase) and glaA promoters.

A protein or fragment thereof encoding nucleic acid molecule of the present invention may also be operably linked to a terminator sequence at its 3' terminus. The terminator sequence

5   may be native to the nucleic acid sequence encoding the protein or fragment thereof or may be obtained from foreign sources. Any terminator which is functional in the fungal host cell of choice may be used in the present invention, but particularly preferred terminators are obtained from the genes encoding *Aspergillus oryzae* TAKA amylase, *Aspergillus niger* glucoamylase, *Aspergillus nidulans* anthranilate synthase, *Aspergillus niger* alpha-glucosidase and

10   *Saccharomyces cerevisiae* enolase.

A protein or fragment thereof encoding nucleic acid molecule of the present invention may also be operably linked to a suitable leader sequence. A leader sequence is a nontranslated region of a mRNA which is important for translation by the fungal host. The leader sequence is operably linked to the 5' terminus of the nucleic acid sequence encoding the protein or fragment

15   thereof. The leader sequence may be native to the nucleic acid sequence encoding the protein or fragment thereof or may be obtained from foreign sources. Any leader sequence which is functional in the fungal host cell of choice may be used in the present invention, but particularly preferred leaders are obtained from the genes encoding *Aspergillus oryzae* TAKA amylase and *Aspergillus oryzae* triose phosphate isomerase.

20   A polyadenylation sequence may also be operably linked to the 3' terminus of the nucleic acid sequence of the present invention. The polyadenylation sequence is a sequence which when transcribed is recognized by the fungal host to add polyadenosine residues to transcribed mRNA. The polyadenylation sequence may be native to the nucleic acid sequence encoding the protein or

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fragment thereof or may be obtained from foreign sources. Any polyadenylation sequence which is functional in the fungal host of choice may be used in the present invention, but particularly preferred polyadenylation sequences are obtained from the genes encoding *Aspergillus oryzae* TAKA amylase, *Aspergillus niger* glucoamylase, *Aspergillus nidulans* anthranilate synthase and

5   *Aspergillus niger* alpha-glucosidase.

To avoid the necessity of disrupting the cell to obtain the protein or fragment thereof and to minimize the amount of possible degradation of the expressed protein or fragment thereof within the cell, it is preferred that expression of the protein or fragment thereof gives rise to a product secreted outside the cell. To this end, a protein or fragment thereof of the present

10   invention may be linked to a signal peptide linked to the amino terminus of the protein or fragment thereof. A signal peptide is an amino acid sequence which permits the secretion of the protein or fragment thereof from the fungal host into the culture medium. The signal peptide may be native to the protein or fragment thereof of the invention or may be obtained from foreign sources. The 5' end of the coding sequence of the nucleic acid sequence of the present

15   invention may inherently contain a signal peptide coding region naturally linked in translation reading frame with the segment of the coding region which encodes the secreted protein or fragment thereof. Alternatively, the 5' end of the coding sequence may contain a signal peptide coding region which is foreign to that portion of the coding sequence which encodes the secreted protein or fragment thereof. The foreign signal peptide may be required where the coding

20   sequence does not normally contain a signal peptide coding region. Alternatively, the foreign signal peptide may simply replace the natural signal peptide to obtain enhanced secretion of the desired protein or fragment thereof. The foreign signal peptide coding region may be obtained from a glucoamylase or an amylase gene from an *Aspergillus* species, a lipase or proteinase gene

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from *Rhizomucor miehei*, the gene for the alpha-factor from *Saccharomyces cerevisiae*, or the

calf preprochymosin gene. An effective signal peptide for fungal host cells is the *Aspergillus*

oryzae TAKA amylase signal, *Aspergillus niger* neutral amylase signal, the *Rhizomucor miehei*

aspartic proteinase signal, the *Humicola lanuginosus* cellulase signal, or the *Rhizomucor miehei*

5   lipase signal. However, any signal peptide capable of permitting secretion of the protein or

fragment thereof in a fungal host of choice may be used in the present invention.

A protein or fragment thereof encoding nucleic acid molecule of the present invention

may also be linked to a propeptide coding region. A propeptide is an amino acid sequence found

at the amino terminus of aproprotein or proenzyme. Cleavage of the propeptide from the

10   proprotein yields a mature biochemically active protein. The resulting polypeptide is known as a

propolypeptide or proenzyme (or a zymogen in some cases). Propolypeptides are generally

inactive and can be converted to mature active polypeptides by catalytic or autocatalytic cleavage

of the propeptide from the propolypeptide or proenzyme. The propeptide coding region may be

native to the protein or fragment thereof or may be obtained from foreign sources. The foreign

15   propeptide coding region may be obtained from the *Saccharomyces cerevisiae* alpha-factor gene

or *Myceliophthora thermophila* laccase gene (WO 95/33836, the entirety of which is herein

incorporated by reference).

The procedures used to ligate the elements described above to construct the recombinant

expression vector of the present invention are well known to one skilled in the art (see, for

20   example, Sambrook *et al.*, *Molecular Cloning, A Laboratory Manual*, 2nd ed., Cold Spring

Harbor, N.Y., (1989)).

The present invention also relates to recombinant fungal host cells produced by the

methods of the present invention which are advantageously used with the recombinant vector of

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the present invention. The cell is preferably transformed with a vector comprising a nucleic acid sequence of the invention followed by integration of the vector into the host chromosome. The choice of fungal host cells will to a large extent depend upon the gene encoding the protein or fragment thereof and its source. The fungal host cell may, for example, be a yeast cell or a

5 filamentous fungal cell.

"Yeast" as used herein includes *Ascosporogenous* yeast (*Endomycetales*), *Basidiosporogenous* yeast and yeast belonging to the *Fungi Imperfecti* (*Blastomycetes*). The *Ascosporogenous* yeasts are divided into the families *Spermophthoraceae* and *Saccharomycetaceae*. The latter is comprised of four subfamilies, *Schizosaccharomycoideae* (for example, genus *Schizosaccharomyces*), *Nadsonioideae, Lipomycoideae* and *Saccharomycoideae* (for example, genera *Pichia, Kluyveromyces* and *Saccharomyces*). The *Basidiosporogenous* yeasts include the genera *Leucosporidim, Rhodosporidium, Sporidiobolus, Filobasidium* and *Filobasidiella*. Yeast belonging to the *Fungi Imperfecti* are divided into two families, *Sporobolomycetaceae* (for example, genera *Sorobolomyces* and *Bullera*) and *Cryptococcaceae*

15 (for example, genus *Candida*). Since the classification of yeast may change in the future, for the purposes of this invention, yeast shall be defined as described in Biology and Activities of Yeast (Skinner *et al., Soc. App. Bacteriol. Symposium Series* No. 9, (1980), the entirety of which is herein incorporated by reference). The biology of yeast and manipulation of yeast genetics are well known in the art (*see,* for example, *Biochemistry and Genetics of Yeast,* Bacil *et al.* (ed.),

20 2nd edition, 1987; *The Yeasts,* Rose and Harrison (eds.), 2nd ed., (1987); and *The Molecular Biology of the Yeast Saccharomyces,* Strathern *et al.* (eds.), (1981), all of which are herein incorporated by reference in their entirety).

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"Fungi" as used herein includes the phyla *Ascomycota, Basidiomycota, Chytridiomycota* and *Zygomycota* (as defined by Hawksworth *et al.*, In: Ainsworth and Bisby's *Dictionary of The Fungi*, 8th edition, 1995, CAB International, University Press, Cambridge, UK; the entirety of which is herein incorporated by reference) as well as the *Oomycota* (as cited in Hawksworth *et al.*, In: Ainsworth and Bisby's *Dictionary of The Fungi*, 8th edition, 1995, CAB International, University Press, Cambridge, UK) and all mitosporic fungi (Hawksworth *et al.*, In: Ainsworth and Bisby's *Dictionary of The Fungi*, 8th edition, 1995, CAB International, University Press, Cambridge, UK). Representative groups of *Ascomycota* include, for example, *Neurospora, Eupenicillium* (= *Penicillium*), *Emericella* (= *Aspergillus*), *Eurotiun* (= *Aspergillus*) and the true yeasts listed above. Examples of *Basidiomycota* include mushrooms, rusts and smuts. Representative groups of *Chytridiomycota* include, for example, *Allomyces, Blastocladiella, Coelomomyces* and aquatic fungi. Representative groups of *Oomycota* include, for example, *Saprolegniomycetous* aquatic fungi (water molds) such as *Achlya*. Examples of mitosporic fungi include *Aspergillus, Penicillium, Candida* and *Alternaria*. Representative groups of *Zygomycota* include, for example, *Rhizopus* and *Mucor*.

"Filamentous fungi" include all filamentous forms of the subdivision *Eumycota* and *Oomycota* (as defined by Hawksworth *et al.*, In: Ainsworth and Bisby's *Dictionary of The Fungi*, 8th edition, 1995, CAB International, University Press, Cambridge, UK). The filamentous fungi are characterized by a vegetative mycelium composed of chitin, cellulose, glucan, chitosan, mannan and other complex polysaccharides. Vegetative growth is by hyphal elongation and carbon catabolism is obligately aerobic. In contrast, vegetative growth by yeasts such as *Saccharomyces cerevisiae* is by budding of a unicellular thallus and carbon catabolism may be fermentative.

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In one embodiment, the fungal host cell is a yeast cell. In a preferred embodiment, the yeast host cell is a cell of the species of *Candida, Kluyveromyces, Saccharomyces, Schizosaccharomyces, Pichia* and *Yarrowia*. In a preferred embodiment, the yeast host cell is a *Saccharomyces cerevisiae* cell, a *Saccharomyces carlsbergensis, Saccharomyces diastaticus* cell, a *Saccharomyces douglasii* cell, a *Saccharomyces kluyveri* cell, a *Saccharomyces norbensis* cell, or a *Saccharomyces oviformis* cell. In another preferred embodiment, the yeast host cell is a *Kluyveromyces lactis* cell. In another preferred embodiment, the yeast host cell is a *Yarrowia lipolytica* cell.

In another embodiment, the fungal host cell is a filamentous fungal cell. In a preferred embodiment, the filamentous fungal host cell is a cell of the species of, but not limited to, *Acremonium, Aspergillus, Fusarium, Humicola, Myceliophthora, Mucor, Neurospora, Penicillium, Thielavia, Tolypocladium* and *Trichoderma*. In a preferred embodiment, the filamentous fungal host cell is an *Aspergillus* cell. In another preferred embodiment, the filamentous fungal host cell is an *Acremonium* cell. In another preferred embodiment, the filamentous fungal host cell is a *Fusarium* cell. In another preferred embodiment, the filamentous fungal host cell is a *Humicola* cell. In another preferred embodiment, the filamentous fungal host cell is a *Myceliophthora* cell. In another even preferred embodiment, the filamentous fungal host cell is a *Mucor* cell. In another preferred embodiment, the filamentous fungal host cell is a *Neurospora* cell. In another preferred embodiment, the filamentous fungal host cell is a *Penicillium* cell. In another preferred embodiment, the filamentous fungal host cell is a *Thielavia* cell. In another preferred embodiment, the filamentous fungal host cell is a *Tolypocladiun* cell. In another preferred embodiment, the filamentous fungal host cell is a *Trichoderma* cell. In a preferred embodiment, the filamentous fungal host cell is an *Aspergillus*

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oryzae cell, an *Aspergillus niger* cell, an *Aspergillus foetidus* cell, or an *Aspergillus japonicus* cell. In another preferred embodiment, the filamentous fungal host cell is a *Fusarium oxysporum* cell or a *Fusarium graminearum* cell. In another preferred embodiment, the filamentous fungal host cell is a *Humicola insolens* cell or a *Humicola lanuginosus* cell. In another preferred

5   embodiment, the filamentous fungal host cell is a *Myceliophthora thermophila* cell. In a most preferred embodiment, the filamentous fungal host cell is a *Mucor miehei* cell. In a most preferred embodiment, the filamentous fungal host cell is a *Neurospora crassa* cell. In a most preferred embodiment, the filamentous fungal host cell is a *Penicillium purpurogenum* cell. In another most preferred embodiment, the filamentous fungal host cell is a *Thielavia terrestris* cell.

10 In another most preferred embodiment, the *Trichoderma* cell is a *Trichoderma reesei* cell, a *Trichoderna viride* cell, a *Trichoderma longibrachiatum* cell, a *Trichoderma harzianum* cell, or a *Trichoderma koningii* cell. In a preferred embodiment, the fungal host cell is selected from an *A. nidulans* cell, an *A. niger* cell, an *A. oryzae* cell and an *A. sojae* cell. In a further preferred embodiment, the fungal host cell is an *A. nidulans* cell.

15   The recombinant fungal host cells of the present invention may further comprise one or more sequences which encode one or more factors that are advantageous in the expression of the protein or fragment thereof, for example, an activator (e.g., a trans-acting factor), a chaperone and a processing protease. The nucleic acids encoding one or more of these factors are preferably not operably linked to the nucleic acid encoding the protein or fragment thereof. An

20 activator is a protein which activates transcription of a nucleic acid sequence encoding a polypeptide (Kudla *et al., EMBO* 9:1355-1364(1990); Jarai and Buxton, *Current Genetics* 26:2238-244(1994); Verdier, *Yeast* 6:271-297(1990), all of which are herein incorporated by reference in their entirety). The nucleic acid sequence encoding an activator may be obtained

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from the genes encoding *Saccharomyces cerevisiae* heme activator protein 1 (hap1),

Saccharomyces cerevisiae galactose metabolizing protein 4 (gal4) and *Aspergillus nidulans*

ammonia regulation protein (areA). For further examples, see Verdier, *Yeast 6*:271-297 (1990);

MacKenzie *et al.*, *Journal of Gen. Microbiol. 139*:2295-2307 (1993), both of which are herein

5   incorporated by reference in their entirety). A chaperone is a protein which assists another

protein in folding properly (Hartl *et al.*, *TIBS 19*:20-25 (1994); Bergeron *et al.*, *TIBS* 19:124-128

(1994); Demolder *et al.*, *J. Biotechnology* 32:179-189 (1994); Craig, *Science 260*:1902-

1903(1993); Gething and Sambrook, *Nature* 355:33-45 (1992); Puig and Gilbert, *J Biol. Chem.*

269:7764-7771 (1994); Wang and Tsou, *FASEB Journal* 7:1515-11157 (1993); Robinson *et al.*,

10   *Bio/Technology 1*:381-384 (1994), all of which are herein incorporated by reference in their

entirety). The nucleic acid sequence encoding a chaperone may be obtained from the genes

encoding *Aspergillus oryzae* protein disulphide isomerase, *Saccharomyces cerevisiae* calnexin,

Saccharomyces cerevisiae BiP/GRP78 and *Saccharomyces cerevisiae* Hsp70. For further

examples, *see* Gething and Sambrook, *Nature 355*:33-45 (1992); Hartl *et al.*, *TIBS 19*:20-25

15   (1994). A processing protease is a protease that cleaves a propeptide to generate a mature

biochemically active polypeptide (Enderlin and Ogrydziak, *Yeast 10*:67-79 (1994); Fuller *et al.*,

Proc. Natl. Acad. Sci. (U.S.A.) 86:1434-1438 (1989); Julius *et al.*, *Cell 37*:1075-1089 (1984);

Julius *et al.*, *Cell 32*:839-852 (1983), all of which are incorporated by reference in their entirety).

The nucleic acid sequence encoding a processing protease may be obtained from the genes

20   encoding *Aspergillus niger* Kex2, *Saccharomyces cerevisiae* dipeptidylaminopeptidase,

Saccharomyces cerevisiae Kex2 and *Yarrowia lipolytica* dibasic processing endoprotease (xpr6).

Any factor that is functional in the fungal host cell of choice may be used in the present

invention.

Fungal cells may be transformed by a process involving protoplast formation, transformation of the protoplasts and regeneration of the cell wall in a manner known per se. Suitable procedures for transformation of *Aspergillus* host cells are described in EP 238 023 and Yelton *et al.*, *Proc. Natl. Acad. Sci. (U.S.A.)* *81*:1470-1474 (1984), both of which are herein

5   incorporated by reference in their entirety. A suitable method of transforming *Fusarium* species is described by Malardier *et al.*, *Gene 78:*147-156 (1989), the entirety of which is herein incorporated by reference. Yeast may be transformed using the procedures described by Becker and Guarente, In: Abelson and Simon, (eds.), *Guide to Yeast Genetics and Molecular Biology, Methods Enzymol.* Volume 194, pp 182-187, Academic Press, Inc., New York; Ito *et al.*, *J.*

10   *Bacteriology 153*:163 (1983); Hinnen *et al.*, *Proc. Natl. Acad. Sci. (U.S.A.) 75*:1920 (1978), all of which are herein incorporated by reference in their entirety.

       The present invention also relates to methods of producing the protein or fragment thereof comprising culturing the recombinant fungal host cells under conditions conducive for expression of the protein or fragment thereof. The fungal cells of the present invention are

15   cultivated in a nutrient medium suitable for production of the protein or fragment thereof using methods known in the art. For example, the cell may be cultivated by shake flask cultivation, small-scale or large-scale fermentation (including continuous, batch, fed-batch, or solid state fermentations) in laboratory or industrial fermentors performed in a suitable medium and under conditions allowing the protein or fragment thereof to be expressed and/or isolated. The

20   cultivation takes place in a suitable nutrient medium comprising carbon and nitrogen sources and inorganic salts, using procedures known in the art (*see, e.g.*, Bennett and LaSure (eds.), *More Gene Manipulations in Fungi*, Academic Press, CA, (1991), the entirety of which is herein incorporated by reference). Suitable media are available from commercial suppliers or may be

prepared according to published compositions (*e.g.*, in catalogues of the American Type Culture Collection, Manassas, VA). If the protein or fragment thereof is secreted into the nutrient medium, a protein or fragment thereof can be recovered directly from the medium. If the protein or fragment thereof is not secreted, it is recovered from cell lysates.

5   The expressed protein or fragment thereof may be detected using methods known in the art that are specific for the particular protein or fragment. These detection methods may include the use of specific antibodies, formation of an enzyme product, or disappearance of an enzyme substrate. For example, if the protein or fragment thereof has enzymatic activity, an enzyme assay may be used. Alternatively, if polyclonal or monoclonal antibodies specific to the protein

10   or fragment thereof are available, immunoassays may be employed using the antibodies to the protein or fragment thereof. The techniques of enzyme assay and immunoassay are well known to those skilled in the art.

       The resulting protein or fragment thereof may be recovered by methods known in the arts. For example, the protein or fragment thereof may be recovered from the nutrient medium

15   by conventional procedures including, but not limited to, centrifugation, filtration, extraction, spray-drying, evaporation, or precipitation. The recovered protein or fragment thereof may then be further purified by a variety of chromatographic procedures, e.g., ion exchange chromatography, gel filtration chromatography, affinity chromatography, or the like.

(c)   Mammalian Constructs and Transformed Mammalian Cells

20   The present invention also relates to methods for obtaining a recombinant mammalian host cell, comprising introducing into a mammalian host cell exogenous genetic material. The present invention also relates to a mammalian cell comprising a mammalian recombinant vector. The present invention also relates to methods for obtaining a recombinant mammalian host cell,

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comprising introducing into a mammalian cell exogenous genetic material. In a preferred

embodiment the exogenous genetic material includes a nucleic acid molecule of the present

invention having a sequence selected from the group consisting of SEQ ID NO: 1 through SEQ

ID NO: 699 or complements thereof or fragments of either or other nucleic acid molecule of the

5   present invention.

Mammalian cell lines available as hosts for expression are known in the art and include

many immortalized cell lines available from the American Type Culture Collection (ATCC,

Manassas, VA), such as HeLa cells, Chinese hamster ovary (CHO) cells, baby hamster kidney

(BHK) cells and a number of other cell lines. Suitable promoters for mammalian cells are also

10   known in the art and include viral promoters such as that from Simian Virus 40 (SV40) (Fiers *et

al., Nature* 273:113 (1978), the entirety of which is herein incorporated by reference), Rous

sarcoma virus (RSV), adenovirus (ADV) and bovine papilloma virus (BPV). Mammalian cells

may also require terminator sequences and poly-A addition sequences. Enhancer sequences

which increase expression may also be included and sequences which promote amplification of

15   the gene may also be desirable (for example methotrexate resistance genes).

Vectors suitable for replication in mammalian cells may include viral replicons, or

sequences which insure integration of the appropriate sequences encoding HCV epitopes into the

host genome. For example, another vector used to express foreign DNA is vaccinia virus. In this

case, for example, a nucleic acid molecule encoding a protein or fragment thereof is inserted into

20   the vaccinia genome. Techniques for the insertion of foreign DNA into the vaccinia virus

genome are known in the art and may utilize, for example, homologous recombination. Such

heterologous DNA is generally inserted into a gene which is non-essential to the virus, for

example, the thymidine kinase gene (tk), which also provides a selectable marker. Plasmid

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vectors that greatly facilitate the construction of recombinant viruses have been described (*see,* for example, Mackett *et al, J Virol. 49*:857 (1984); Chakrabarti *et al., Mol. Cell. Biol. 5*:3403 (1985); Moss, In: *Gene Transfer Vectors For Mammalian Cells* (Miller and Calos, eds., Cold Spring Harbor Laboratory, N.Y., p. 10, (1987); all of which are herein incorporated by reference

5 in their entirety). Expression of the HCV polypeptide then occurs in cells or animals which are infected with the live recombinant vaccinia virus.

The sequence to be integrated into the mammalian sequence may be introduced into the primary host by any convenient means, which includes calcium precipitated DNA, spheroplast fusion, transformation, electroporation, biolistics, lipofection, microinjection, or other convenient

10 means. Where an amplifiable gene is being employed, the amplifiable gene may serve as the selection marker for selecting hosts into which the amplifiable gene has been introduced. Alternatively, one may include with the amplifiable gene another marker, such as a drug resistance marker, e.g. neomycin resistance (G418 in mammalian cells), hygromycin in resistance etc., or an auxotrophy marker (HIS3, TRP1, LEU2, URA3, ADE2, LYS2, etc.) for use

15 in yeast cells.

Depending upon the nature of the modification and associated targeting construct, various techniques may be employed for identifying targeted integration. Conveniently, the DNA may be digested with one or more restriction enzymes and the fragments probed with an appropriate DNA fragment which will identify the properly sized restriction fragment associated with

20 integration.

One may use different promoter sequences, enhancer sequences, or other sequence which will allow for enhanced levels of expression in the expression host. Thus, one may combine an enhancer from one source, a promoter region from another source, a 5'- noncoding region

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upstream from the initiation methionine from the same or different source as the other sequences and the like. One may provide for an intron in the non-coding region with appropriate splice sites or for an alternative 3'- untranslated sequence or polyadenylation site. Depending upon the particular purpose of the modification, any of these sequences may be introduced, as desired.

5   Where selection is intended, the sequence to be integrated will have with it a marker gene, which allows for selection. The marker gene may conveniently be downstream from the target gene and may include resistance to a cytotoxic agent, e.g. antibiotics, heavy metals, or the like, resistance or susceptibility to HAT, gancyclovir, etc., complementation to an auxotrophic host, particularly by using an auxotrophic yeast as the host for the subject manipulations, or the

10   like. The marker gene may also be on a separate DNA molecule, particularly with primary mammalian cells. Alternatively, one may screen the various transformants, due to the high efficiency of recombination in yeast, by using hybridization analysis, PCR, sequencing, or the like.

For homologous recombination, constructs can be prepared where the amplifiable gene

15   will be flanked, normally on both sides with DNA homologous with the DNA of the target region. Depending upon the nature of the integrating DNA and the purpose of the integration, the homologous DNA will generally be within 100kb, usually 50kb, preferably about 25kb, of the transcribed region of the target gene, more preferably within 2kb of the target gene. Where modeling of the gene is intended, homology will usually be present proximal to the site of the

20   mutation. The homologous DNA may include the 5'-upstream region outside of the transcriptional regulatory region or comprising any enhancer sequences, transcriptional initiation sequences, adjacent sequences, or the like. The homologous region may include a portion of the coding region, where the coding region may be comprised only of an open reading frame or

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combination of exons and introns. The homologous region may comprise all or a portion of an intron, where all or a portion of one or more exons may also be present. Alternatively, the homologous region may comprise the 3'-region, so as to comprise all or a portion of the transcriptional termination region, or the region 3' of this region. The homologous regions may

5   extend over all or a portion of the target gene or be outside the target gene comprising all or a portion of the transcriptional regulatory regions and/or the structural gene.

The integrating constructs may be prepared in accordance with conventional ways, where sequences may be synthesized, isolated from natural sources, manipulated, cloned, ligated, subjected to in vitro mutagenesis, primer repair, or the like. At various stages, the joined

10   sequences may be cloned and analyzed by restriction analysis, sequencing, or the like. Usually during the preparation of a construct where various fragments are joined, the fragments, intermediate constructs and constructs will be carried on a cloning vector comprising a replication system functional in a prokaryotic host, e.g., *E. coli* and a marker for selection, e.g., biocide resistance, complementation to an auxotrophic host, etc. Other functional sequences may

15   also be present, such as polylinkers, for ease of introduction and excision of the construct or portions thereof, or the like. A large number of cloning vectors are available such as pBR322, the pUC series, etc. These constructs may then be used for integration into the primary mammalian host.

In the case of the primary mammalian host, a replicating vector may be used. Usually,

20   such vector will have a viral replication system, such as SV40, bovine papilloma virus, adenovirus, or the like. The linear DNA sequence vector may also have a selectable marker for identifying transfected cells. Selectable markers include the neo gene, allowing for selection

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with G418, the herpes tk gene for selection with HAT medium, the gpt gene with mycophenolic acid, complementation of an auxotrophic host, etc.

The vector may or may not be capable of stable maintenance in the host. Where the vector is capable of stable maintenance, the cells will be screened for homologous integration of the vector into the genome of the host, where various techniques for curing the cells may be employed. Where the vector is not capable of stable maintenance, for example, where a temperature sensitive replication system is employed, one may change the temperature from the permissive temperature to the non-permissive temperature, so that the cells may be cured of the vector. In this case, only those cells having integration of the construct comprising the amplifiable gene and, when present, the selectable marker, will be able to survive selection.

Where a selectable marker is present, one may select for the presence of the targeting construct by means of the selectable marker. Where the selectable marker is not present, one may select for the presence of the construct by the amplifiable gene. For the neo gene or the herpes tk gene, one could employ a medium for growth of the transformants of about 0.1-1 mg/ml of G418 or may use HAT medium, respectively. Where DHFR is the amplifiable gene, the selective medium may include from about 0.01-0.5 μM of methotrexate or be deficient in glycine-hypoxanthine-thymidine and have dialysed serum (GHT media).

The DNA can be introduced into the expression host by a variety of techniques that include calcium phosphate/DNA co-precipitates, microinjection of DNA into the nucleus, electroporation, yeast protoplast fusion with intact cells, transfection, polycations, e.g., polybrene, polyornithine, etc., or the like. The DNA may be single or double stranded DNA, linear or circular. The various techniques for transforming mammalian cells are well known (see Keown *et al.*, *Methods Enzymol.* (1989); Keown *et al.*, *Methods Enzymol.* *185*:527-537 (1990);

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Mansour *et al.*, *Nature 336*:348-352, (1988); all of which are herein incorporated by reference in their entirety).

(d) Insect Constructs and Transformed Insect Cells

The present invention also relates to an insect recombinant vectors comprising exogenous

5   genetic material. The present invention also relates to an insect cell comprising an insect

recombinant vector. The present invention also relates to methods for obtaining a recombinant

insect host cell, comprising introducing into an insect cell exogenous genetic material. In a

preferred embodiment the exogenous genetic material includes a nucleic acid molecule of the

present invention having a sequence selected from the group consisting of SEQ ID NO: 1

10   through SEQ ID NO: 699 or complements thereof or fragments of either or other nucleic acid

molecule of the present invention.

The insect recombinant vector may be any vector which can be conveniently subjected to

recombinant DNA procedures and can bring about the expression of the nucleic acid sequence.

The choice of a vector will typically depend on the compatibility of the vector with the insect

15   host cell into which the vector is to be introduced. The vector may be a linear or a closed circular

plasmid. The vector system may be a single vector or plasmid or two or more vectors or

plasmids which together contain the total DNA to be introduced into the genome of the insect

host. In addition, the insect vector may be an expression vector. Nucleic acid molecules can be

suitably inserted into a replication vector for expression in the insect cell under a suitable

20   promoter for insect cells. Many vectors are available for this purpose and selection of the

appropriate vector will depend mainly on the size of the nucleic acid molecule to be inserted into

the vector and the particular host cell to be transformed with the vector. Each vector contains

various components depending on its function (amplification of DNA or expression of DNA) and

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the particular host cell with which it is compatible. The vector components for insect cell

transformation generally include, but are not limited to, one or more of the following: a signal

sequence, origin of replication, one or more marker genes and an inducible promoter.

The insect vector may be an autonomously replicating vector, *i.e.*, a vector which exists

as an extrachromosomal entity, the replication of which is independent of chromosomal

replication, *e.g.*, a plasmid, an extrachromosomal element, a minichromosome, or an artificial

chromosome. The vector may contain any means for assuring self-replication. Alternatively, the

vector may be one which, when introduced into the insect cell, is integrated into the genome and

replicated together with the chromosome(s) into which it has been integrated. For integration,

the vector may rely on the nucleic acid sequence of the vector for stable integration of the vector

into the genome by homologous or nonhomologous recombination. Alternatively, the vector

may contain additional nucleic acid sequences for directing integration by homologous

recombination into the genome of the insect host. The additional nucleic acid sequences enable

the vector to be integrated into the host cell genome at a precise location(s) in the

chromosome(s). To increase the likelihood of integration at a precise location, there should be

preferably two nucleic acid sequences which individually contain a sufficient number of nucleic

acids, preferably 400bp to 1500bp, more preferably 800bp to 1000bp, which are highly

homologous with the corresponding target sequence to enhance the probability of homologous

recombination. These nucleic acid sequences may be any sequence that is homologous with a

target sequence in the genome of the insect host cell and, furthermore, may be non-encoding or

encoding sequences.

Baculovirus expression vectors (BEVs) have become important tools for the expression

of foreign genes, both for basic research and for the production of proteins with direct clinical

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applications in human and veterinary medicine (Doerfler, *Curr. Top. Microbiol. Immunol.* *131*:51-68 (1968); Luckow and Summers, *Bio/Technology 6*:47-55 (1988a); Miller, *Annual Review of Microbiol. 42*:177-199 (1988); Summers, *Curr. Comm. Molecular Biology*, Cold Spring Harbor Press, Cold Spring Harbor, N.Y. (1988); all of which are herein incorporated by

5   reference in their entirety). BEVs are recombinant insect viruses in which the coding sequence for a chosen foreign gene has been inserted behind a baculovirus promoter in place of the viral gene, e.g., polyhedrin (Smith and Summers, U.S. Pat. No., 4,745,051, the entirety of which is incorporated herein by reference).

The use of baculovirus vectors relies upon the host cells being derived from *Lepidopteran*

10   insects such as *Spodoptera frugiperda* or *Trichoplusia ni*. The preferred *Spodoptera frugiperda* cell line is the cell line Sf9. The *Spodoptera frugiperda* Sf9 cell line was obtained from American Type Culture Collection (Manassas, VA.) and is assigned accession number ATCC CRL 1711 (Summers and Smith, *A Manual of Methods for Baculovirus Vectors and Insect Cell Culture Procedures,* Texas Ag. Exper. Station Bulletin No. 1555 (1988), the entirety of which is

15   herein incorporated by reference). Other insect cell systems, such as the silkworm *B. mori* may also be used.

The proteins expressed by the BEVs are, therefore, synthesized, modified and transported in host cells derived from *Lepidopteran* insects. Most of the genes that have been inserted and produced in the baculovirus expression vector system have been derived from vertebrate species.

20   Other baculovirus genes in addition to the polyhedrin promoter may be employed to advantage in a baculovirus expression system. These include immediate-early (alpha), delayed-early (β), late (γ), or very late (delta), according to the phase of the viral infection during which they are expressed. The expression of these genes occurs sequentially, probably as the result of a

"cascade" mechanism of transcriptional regulation. (Guarino and Summers, *J. Virol. 57*:563-571 (1986); Guarino and Summers, *J. Virol. 61*:2091-2099 (1987); Guarino and Summers, *Virol. 162*:444-451 (1988); all of which are herein incorporated by reference in their entirety).

Insect recombinant vectors are useful as intermediates for the infection or transformation

5   of insect cell systems. For example, an insect recombinant vector containing a nucleic acid molecule encoding a baculovirus transcriptional promoter followed downstream by an insect signal DNA sequence is capable of directing the secretion of the desired biologically active protein from the insect cell. The vector may utilize a baculovirus transcriptional promoter region derived from any of the over 500 baculoviruses generally infecting insects, such as for example

10   the Orders *Lepidoptera, Diptera, Orthoptera, Coleoptera and Hymenoptera*, including for example but not limited to the viral DNAs of *Autographa californica MNPV, Bombyx mori NPV, Trichoplusia ni MNPV, Rachiplusia ou MNPV or Galleria mellonella MNPV*, wherein said baculovirus transcriptional promoter is a baculovirus immediate-early gene IE1 or IEN promoter; an immediate-early gene in combination with a baculovirus delayed-early gene promoter region

15   selected from the group consisting of 39K and a *HindIII-k* fragment delayed-early gene; or a baculovirus late gene promoter. The immediate-early or delayed-early promoters can be enhanced with transcriptional enhancer elements. The insect signal DNA sequence may code for a signal peptide of a *Lepidopteran* adipokinetic hormone precursor or a signal peptide of the *Manduca sexta* adipokinetic hormone precursor (Summers, U.S. Patent No. 5,155,037; the

20   entirety of which is herein incorporated by reference). Other insect signal DNA sequences include a signal peptide of the *Orthoptera Schistocerca gregaria* locust adipokinetic hormone precurser and the *Drosophila melanogaster* cuticle genes CP1, CP2, CP3 or CP4 or for an insect

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signal peptide having substantially a similar chemical composition and function (Summers, U.S. Patent No. 5,155,037).

Insect cells are distinctly different from animal cells. Insects have a unique life cycle and have distinct cellular properties such as the lack of intracellular plasminogen activators in which are present in vertebrate cells. Another difference is the high expression levels of protein products ranging from 1 to greater than 500 mg/liter and the ease at which cDNA can be cloned into cells (Frasier, *In Vitro Cell. Dev. Biol.* 25:225 (1989); Summers and Smith, In: *A Manual of Methods for Baculovirus Vectors and Insect Cell Culture Procedures,* Texas Ag. Exper. Station Bulletin No. 1555 (1988), both of which are incorporated by reference in their entirety).

Recombinant protein expression in insect cells is achieved by viral infection or stable transformation. For viral infection, the desired gene is cloned into baculovirus at the site of the wild-type polyhedron gene (Webb and Summers, *Technique* 2:173 (1990); Bishop and Posse, *Adv. Gene Technol.* 1:55 (1990); both of which are incorporated by reference in their entirety). The polyhedron gene is a component of a protein coat in occlusions which encapsulate virus particles. Deletion or insertion in the polyhedron gene results the failure to form occlusion bodies. Occlusion negative viruses are morphologically different from occlusion positive viruses and enable one skilled in the art to identify and purify recombinant viruses.

The vectors of present invention preferably contain one or more selectable markers which permit easy selection of transformed cells. A selectable marker is a gene the product of which provides, for example biocide or viral resistance, resistance to heavy metals, prototrophy to auxotrophs and the like. Selection may be accomplished by co-transformation, *e.g.*, as described in WO 91/17243, a nucleic acid sequence of the present invention may be operably linked to a suitable promoter sequence. The promoter sequence is a nucleic acid sequence which is

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recognized by the insect host cell for expression of the nucleic acid sequence. The promoter sequence contains transcription and translation control sequences which mediate the expression of the protein or fragment thereof. The promoter may be any nucleic acid sequence which shows transcriptional activity in the insect host cell of choice and may be obtained from genes encoding

5   polypeptides either homologous or heterologous to the host cell.

For example, a nucleic acid molecule encoding a protein or fragment thereof may also be operably linked to a suitable leader sequence. A leader sequence is a nontranslated region of a mRNA which is important for translation by the fungal host. The leader sequence is operably linked to the 5' terminus of the nucleic acid sequence encoding the protein or fragment thereof.

10   The leader sequence may be native to the nucleic acid sequence encoding the protein or fragment thereof or may be obtained from foreign sources. Any leader sequence which is functional in the insect host cell of choice may be used in the present invention.

A polyadenylation sequence may also be operably linked to the 3' terminus of the nucleic acid sequence of the present invention. The polyadenylation sequence is a sequence which when

15   transcribed is recognized by the insect host to add polyadenosine residues to transcribed mRNA. The polyadenylation sequence may be native to the nucleic acid sequence encoding the protein or fragment thereof or may be obtained from foreign sources. Any polyadenylation sequence which is functional in the fungal host of choice may be used in the present invention.

To avoid the necessity of disrupting the cell to obtain the protein or fragment thereof and

20   to minimize the amount of possible degradation of the expressed polypeptide within the cell, it is preferred that expression of the polypeptide gene gives rise to a product secreted outside the cell. To this end, the protein or fragment thereof of the present invention may be linked to a signal peptide linked to the amino terminus of the protein or fragment thereof. A signal peptide is an

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amino acid sequence which permits the secretion of the protein or fragment thereof from the insect host into the culture medium. The signal peptide may be native to the protein or fragment thereof of the invention or may be obtained from foreign sources. The 5' end of the coding sequence of the nucleic acid sequence of the present invention may inherently contain a signal

5   peptide coding region naturally linked in translation reading frame with the segment of the coding region which encodes the secreted protein or fragment thereof.

At present, a mode of achieving secretion of a foreign gene product in insect cells is by way of the foreign gene's native signal peptide. Because the foreign genes are usually from non-insect organisms, their signal sequences may be poorly recognized by insect cells and hence,

10   levels of expression may be suboptimal. However, the efficiency of expression of foreign gene products seems to depend primarily on the characteristics of the foreign protein. On average, nuclear localized or non-structural proteins are most highly expressed, secreted proteins are intermediate and integral membrane proteins are the least expressed. One factor generally affecting the efficiency of the production of foreign gene products in a heterologous host system

15   is the presence of native signal sequences (also termed presequences, targeting signals, or leader sequences) associated with the foreign gene. The signal sequence is generally coded by a DNA sequence immediately following (5' to 3') the translation start site of the desired foreign gene.

The expression dependence on the type of signal sequence associated with a gene product can be represented by the following example: If a foreign gene is inserted at a site downstream

20   from the translational start site of the baculovirus polyhedrin gene so as to produce a fusion protein (containing the N-terminus of the polyhedrin structural gene), the fused gene is highly expressed. But less expression is achieved when a foreign gene is inserted in a baculovirus

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expression vector immediately following the transcriptional start site and totally replacing the polyhedrin structural gene.

Insertions into the region -50 to -1 significantly alter (reduce) steady state transcription which, in turn, reduces translation of the foreign gene product. Use of the pVL941 vector optimizes transcription of foreign genes to the level of the polyhedrin gene transcription. Even though the transcription of a foreign gene may be optimal, optimal translation may vary because of several factors involving processing: signal peptide recognition, mRNA and ribosome binding, glycosylation, disulfide bond formation, sugar processing, oligomerization, for example.

The properties of the insect signal peptide are expected to be more optimal for the efficiency of the translation process in insect cells than those from vertebrate proteins. This phenomenon can generally be explained by the fact that proteins secreted from cells are synthesized as precursor molecules containing hydrophobic N-terminal signal peptides. The signal peptides direct transport of the select protein to its target membrane and are then cleaved by a peptidase on the membrane, such as the endoplasmic reticulum, when the protein passes through it.

Another exemplary insect signal sequence is the sequence encoding for Drosophila cuticle proteins such as CP1, CP2, CP3 or CP4 (Summers, U.S. Patent No. 5,278,050; the entirety of which is herein incorporated by reference). Most of a 9kb region of the Drosophila genome containing genes for the cuticle proteins has been sequenced. Four of the five cuticle genes contains a signal peptide coding sequence interrupted by a short intervening sequence (about 60 base pairs) at a conserved site. Conserved sequences occur in the 5' mRNA untranslated region, in the adjacent 35 base pairs of upstream flanking sequence and at -200 base pairs from the mRNA start position in each of the cuticle genes.

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Standard methods of insect cell culture, cotransfection and preparation of plasmids are set forth in Summers and Smith (Summers and Smith, *A Manual of Methods for Baculovirus Vectors and Insect Cell Culture Procedures*, Texas Agricultural Experiment Station Bulletin No. 1555, Texas A&M University (1987)). Procedures for the cultivation of viruses and cells are described in Volkman and Summers, *J. Virol* 19:820-832 (1975) and Volkman *et al.*, *J. Virol* 19:820-832 (1976); both of which are herein incorporated by reference in their entirety.

(e)   Bacterial Constructs and Transformed Bacterial Cells

The present invention also relates to a bacterial recombinant vector comprising exogenous genetic material. The present invention also relates to a bacteria cell comprising a bacterial recombinant vector. The present invention also relates to methods for obtaining a recombinant bacteria host cell, comprising introducing into a bacterial host cell exogenous genetic material. . In a preferred embodiment the exogenous genetic material includes a nucleic acid molecule of the present invention having a sequence selected from the group consisting of SEQ ID NO: 1 through SEQ ID NO: 699 or complements thereof or fragments of either or other nucleic acid molecule of the present invention.

The bacterial recombinant vector may be any vector which can be conveniently subjected to recombinant DNA procedures. The choice of a vector will typically depend on the compatibility of the vector with the bacterial host cell into which the vector is to be introduced. The vector may be a linear or a closed circular plasmid. The vector system may be a single vector or plasmid or two or more vectors or plasmids which together contain the total DNA to be introduced into the genome of the bacterial host. In addition, the bacterial vector may be an expression vector. Nucleic acid molecules encoding protein homologues or fragments thereof can, for example, be suitably inserted into a replicable vector for expression in the bacterium

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under the control of a suitable promoter for bacteria. Many vectors are available for this purpose and selection of the appropriate vector will depend mainly on the size of the nucleic acid to be inserted into the vector and the particular host cell to be transformed with the vector. Each vector contains various components depending on its function (amplification of DNA or

5   expression of DNA) and the particular host cell with which it is compatible. The vector components for bacterial transformation generally include, but are not limited to, one or more of the following: a signal sequence, an origin of replication, one or more marker genes and an inducible promoter.

In general, plasmid vectors containing replicon and control sequences that are derived

10   from species compatible with the host cell are used in connection with bacterial hosts. The vector ordinarily carries a replication site, as well as marking sequences that are capable of providing phenotypic selection in transformed cells. For example, *E. coli* is typically transformed using pBR322, a plasmid derived from an *E. coli* species (see, e.g., Bolivar *et al.*, *Gene* 2:95 (1977); the entirety of which is herein incorporated by reference). pBR322 contains

15   genes for ampicillin and tetracycline resistance and thus provides easy means for identifying transformed cells. The pBR322 plasmid, or other microbial plasmid or phage, also generally contains, or is modified to contain, promoters that can be used by the microbial organism for expression of the selectable marker genes.

Nucleic acid molecules encoding protein or fragments thereof may be expressed not only

20   directly, but also as a fusion with another polypeptide, preferably a signal sequence or other polypeptide having a specific cleavage site at the N-terminus of the mature polypeptide. In general, the signal sequence may be a component of the vector, or it may be a part of the polypeptide DNA that is inserted into the vector. The heterologous signal sequence selected

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should be one that is recognized and processed (i.e., cleaved by a signal peptidase) by the host cell. For bacterial host cells that do not recognize and process the native polypeptide signal sequence, the signal sequence is substituted by a bacterial signal sequence selected, for example, from the group consisting of the alkaline phosphatase, penicillinase, lpp, or heat-stable

5   enterotoxin II leaders.

Both expression and cloning vectors contain a nucleic acid sequence that enables the vector to replicate in one or more selected host cells. Generally, in cloning vectors this sequence is one that enables the vector to replicate independently of the host chromosomal DNA and includes origins of replication or autonomously replicating sequences. Such sequences are well

10   known for a variety of bacteria. The origin of replication from the plasmid pBR322 is suitable for most Gram-negative bacteria.

Expression and cloning vectors also generally contain a selection gene, also termed a selectable marker. This gene encodes a protein necessary for the survival or growth of transformed host cells grown in a selective culture medium. Host cells not transformed with the

15   vector containing the selection gene will not survive in the culture medium. Typical selection genes encode proteins that (a) confer resistance to antibiotics or other toxins, e.g., ampicillin, neomycin, methotrexate, or tetracycline, (b) complement auxotrophic deficiencies, or (c) supply critical nutrients not available from complex media, e.g., the gene encoding D-alanine racemase for *Bacilli*. One example of a selection scheme utilizes a drug to arrest growth of a host cell.

20   Those cells that are successfully transformed with a heterologous protein homologue or fragment thereof produce a protein conferring drug resistance and thus survive the selection regimen.

The expression vector for producing a protein or fragment thereof can also contains an inducible promoter that is recognized by the host bacterial organism and is operably linked to the

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nucleic acid encoding, for example, the nucleic acid molecule encoding the protein homologue or

fragment thereof of interest. Inducible promoters suitable for use with bacterial hosts include the

β-lactamase and lactose promoter systems (Chang *et al.*, *Nature 275*:615 (1978); Goeddel *et al.*,

Nature 281:544 (1979); both of which are herein incorporated by reference in their entirety), the

5   arabinose promoter system (Guzman *et al.*, *J. Bacteriol. 174*:7716-7728 (1992); the entirety of

which is herein incorporated by reference), alkaline phosphatase, a tryptophan (trp) promoter

system (Goeddel, *Nucleic Acids Res. 8*:4057 (1980); EP 36,776; both of which are herein

incorporated by reference in their entirety) and hybrid promoters such as the tac promoter

(deBoer *et al.*, *Proc. Natl. Acad. Sci. (USA) 80*:21-25 (1983); the entirety of which is herein

10   incorporated by reference). However, other known bacterial inducible promoters are suitable

(Siebenlist *et al.*, *Cell 20*:269 (1980); the entirety of which is herein incorporated by reference).

Promoters for use in bacterial systems also generally contain a Shine-Dalgarno (S.D.)

sequence operably linked to the DNA encoding the polypeptide of interest. The promoter can be

removed from the bacterial source DNA by restriction enzyme digestion and inserted into the

15   vector containing the desired DNA.

Construction of suitable vectors containing one or more of the above-listed components

employs standard ligation techniques. Isolated plasmids or DNA fragments are cleaved, tailored

and re-ligated in the form desired to generate the plasmids required. Examples of available

bacterial expression vectors include, but are not limited to, the multifunctional *E. coli* cloning

20   and expression vectors such as Bluescript™ (Stratagene, La Jolla, CA), in which, for example,

encoding an *A. nidulans* protein homologue or fragment thereof homologue, may be ligated into

the vector in frame with sequences for the amino-terminal Met and the subsequent 7 residues of

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β-galactosidase so that a hybrid protein is produced; pIN vectors (Van Heeke and Schuster, *J. Biol. Chem. 264*:5503-5509 (1989), the entirety of which is herein incorporated by reference); and the like. pGEX vectors (Promega, Madison Wisconsin U.S.A.) may also be used to express foreign polypeptides as fusion proteins with glutathione S-transferase (GST). In general, such

5   fusion proteins are soluble and can easily be purified from lysed cells by adsorption to glutathione-agarose beads followed by elution in the presence of free glutathione. Proteins made in such systems are designed to include heparin, thrombin or factor XA protease cleavage sites so that the cloned polypeptide of interest can be released from the GST moiety at will.

Suitable host bacteria for a bacterial vector include archaebacteria and eubacteria,

10   especially eubacteria and most preferably *Enterobacteriaceae*. Examples of useful bacteria include *Escherichia, Enterobacter, Azotobacter, Erwinia, Bacillus, Pseudomonas, Klebsiella, Proteus, Salmonella, Serratia, Shigella, Rhizobia, Vitreoscilla and Paracoccus*. Suitable *E. coli* hosts include *E. coli* W3110 (American Type Culture Collection (ATCC) 27,325, Manassas, Virginia U.S.A.), *E. coli* 294 (ATCC 31,446), *E. coli* B and *E. coli* X1776 (ATCC 31,537).

15   These examples are illustrative rather than limiting. Mutant cells of any of the above-mentioned bacteria may also be employed. It is, of course, necessary to select the appropriate bacteria taking into consideration replicability of the replicon in the cells of a bacterium. For example, *E. coli, Serratia*, or *Salmonella* species can be suitably used as the host when well known plasmids such as pBR322, pBR325, pACYC177, or pKN410 are used to supply the replicon. *E. coli* strain

20   W3110 is a preferred host or parent host because it is a common host strain for recombinant DNA product fermentations. Preferably, the host cell should secrete minimal amounts of proteolytic enzymes.

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Host cells are transfected and preferably transformed with the above-described vectors and cultured in conventional nutrient media modified as appropriate for inducing promoters, selecting transformants, or amplifying the genes encoding the desired sequences.

5   Numerous methods of transfection are known to the ordinarily skilled artisan, for example, calcium phosphate and electroporation. Depending on the host cell used, transformation is done using standard techniques appropriate to such cells. The calcium treatment employing calcium chloride, as described in section 1.82 of Sambrook *et al.*, *Molecular Cloning: A Laboratory Manual*, New York: Cold Spring Harbor Laboratory Press, (1989), is generally used for bacterial cells that contain substantial cell-wall barriers. Another

10   method for transformation employs polyethylene glycol/DMSO, as described in Chung and Miller (Chung and Miller, *Nucleic Acids Res. 16*:3580 (1988); the entirety of which is herein incorporated by reference). Yet another method is the use of the technique termed electroporation.

Bacterial cells used to produce the polypeptide of interest for purposes of this invention

15   are cultured in suitable media in which the promoters for the nucleic acid encoding the heterologous polypeptide can be artificially induced as described generally, e.g., in Sambrook *et al.*, *Molecular Cloning: A Laboratory Manual*, New York: Cold Spring Harbor Laboratory Press, (1989). Examples of suitable media are given in U.S. Pat. Nos. 5,304,472 and 5,342,763; both of which are incorporated by reference in their entirety.

20   In addition to the above discussed procedures, practitioners are familiar with the standard resource materials which describe specific conditions and procedures for the construction, manipulation and isolation of macromolecules (e.g., DNA molecules, plasmids, etc.), generation of recombinant organisms and the screening and isolating of clones, (see for example, Sambrook

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et al., Molecular Cloning: A Laboratory Manual, Cold Spring Harbor Press (1989); Mailga *et al., Methods in Plant Molecular Biology,* Cold Spring Harbor Press (1995), the entirety of which is herein incorporated by reference; Birren *et al., Genome Analysis: Analyzing DNA,* 1, Cold Spring Harbor, New York, the entirety of which is herein incorporated by reference).

5   **(f)   Computer Readable Media**

The nucleotide sequence provided in SEQ ID NO: 1 through SEQ ID NO: 699 or fragment thereof, or complement thereof, or a nucleotide sequence at least 90% identical, preferably 95%, identical even more preferably 99% or 100% identical to the sequence provided in SEQ ID NO: 1 through SEQ ID NO: 699 or fragment thereof, or complement thereof, can be

10   "provided" in a variety of mediums to facilitate use. Such a medium can also provide a subset thereof in a form that allows a skilled artisan to examine the sequences.

A preferred subset of nucleotide sequences are those nucleic acid sequences that encode a first nucleic acid molecule selected from the group consisting of a nucleic acid molecule that encodes a maize or soybean glucose-6-phosphate-1-dehydrogenase enzyme or complement

15   thereof or fragment of either; a nucleic acid molecule that encodes a maize or soybean 6-phosphogluconate dehydrogenase enzyme or complement thereof or fragment of either; a nucleic acid molecule that encodes a putative maize or soybean 6-phosphogluconate dehydrogenase enzyme or complement thereof or fragment of either; a nucleic acid molecule that encodes a maize or soybean D-ribulose-5-phosphate-3-epimerase enzyme or complement thereof or

20   fragment of either; a nucleic acid molecule that encodes a maize or soybean ribose-5-phosphate isomerase enzyme or complement thereof or fragment of either; a nucleic acid molecule that encodes a putative maize or soybean ribose-5-phosphate isomerase enzyme or complement thereof or fragment of either; a nucleic acid molecule that encodes a maize or soybean

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transketolase enzyme or complement thereof or fragment of either; a nucleic acid molecule that encodes a putative maize or soybean transketolase enzyme or complement thereof or fragment of either; a nucleic acid molecule that encodes a maize or soybean transaldolase enzyme or complement thereof or fragment of either; a nucleic acid molecule that encodes a putative maize transaldolase enzyme or complement thereof or fragment of either; and a nucleic acid molecule that encodes a maize or soybean phosphoglucoisomerase enzyme or complement thereof or fragment of either.

A further preferred subset of nucleic acid sequences is where the subset of sequences which encode two proteins or fragments thereof, more preferably three proteins or fragments thereof, more preferable four proteins or fragments thereof, more preferably five proteins or fragments thereof, more preferably six proteins or fragments thereof, more preferably seven proteins or fragments thereof, more preferably eight proteins or fragments thereof, more preferably nine proteins or fragments thereof, more preferably ten proteins or fragments thereof, and even more preferably eleven proteins or fragments thereof. These nucleic acid sequences are selected from the group that encodes a maize or soybean glucose-6-phosphate-1-dehydrogenase enzyme or complement thereof or fragment of either; a nucleic acid molecule that encodes a maize or soybean 6-phosphogluconate dehydrogenase enzyme or complement thereof or fragment of either; a nucleic acid molecule that encodes a putative maize or soybean 6-phosphogluconate dehydrogenase enzyme or complement thereof or fragment of either; a nucleic acid molecule that encodes a maize or soybean D-ribulose-5-phosphate-3-epimerase enzyme or complement thereof or fragment of either; a nucleic acid molecule that encodes a maize or soybean ribose-5-phosphate isomerase enzyme or complement thereof or fragment of either; a nucleic acid molecule that encodes a putative maize or soybean ribose-5-phosphate isomerase

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enzyme or complement thereof or fragment of either; a nucleic acid molecule that encodes a maize or soybean transketolase enzyme or complement thereof or fragment of either; a nucleic acid molecule that encodes a putative maize or soybean transketolase enzyme or complement thereof or fragment of either; a nucleic acid molecule that encodes a maize or soybean

5   transaldolase enzyme or complement thereof or fragment of either; a nucleic acid molecule that encodes a putative maize transaldolase enzyme or complement thereof or fragment of either; and a nucleic acid molecule that encodes a maize or soybean phosphoglucoisomerase enzyme or complement thereof or fragment of either.

In one application of this embodiment, a nucleotide sequence of the present invention can

10   be recorded on computer readable media. As used herein, "computer readable media" refers to any medium that can be read and accessed directly by a computer. Such media include, but are not limited to: magnetic storage media, such as floppy discs, hard disc, storage medium and magnetic tape: optical storage media such as CD-ROM; electrical storage media such as RAM and ROM; and hybrids of these categories such as magnetic/optical storage media. A skilled

15   artisan can readily appreciate how any of the presently known computer readable mediums can be used to create a manufacture comprising computer readable medium having recorded thereon a nucleotide sequence of the present invention.

As used herein, "recorded" refers to a process for storing information on computer readable medium. A skilled artisan can readily adopt any of the presently known methods for

20   recording information on computer readable medium to generate media comprising the nucleotide sequence information of the present invention. A variety of data storage structures are available to a skilled artisan for creating a computer readable medium having recorded thereon a nucleotide sequence of the present invention. The choice of the data storage structure will

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generally be based on the means chosen to access the stored information. In addition, a variety of data processor programs and formats can be used to store the nucleotide sequence information of the present invention on computer readable medium. The sequence information can be represented in a word processing text file, formatted in commercially-available software such as

5   WordPerfect and Microsoft Word, or represented in the form of an ASCII file, stored in a database application, such as DB2, Sybase, Oracle, or the like. A skilled artisan can readily adapt any number of data processor structuring formats (e.g. text file or database) in order to obtain computer readable medium having recorded thereon the nucleotide sequence information of the present invention.

10   By providing one or more of nucleotide sequences of the present invention, a skilled artisan can routinely access the sequence information for a variety of purposes. Computer software is publicly available which allows a skilled artisan to access sequence information provided in a computer readable medium. The examples which follow demonstrate how software which implements the BLAST (Altschul *et al., J. Mol. Biol. 215:*403-410 (1990), the

15   entirety of which is herein incorporated by reference) and BLAZE (Brutlag *et al., Comp. Chem. 17:*203-207 (1993), the entirety of which is herein incorporated by reference) search algorithms on a Sybase system can be used to identify open reading frames (ORFs) within the genome that contain homology to ORFs or proteins from other organisms. Such ORFs are protein-encoding fragments within the sequences of the present invention and are useful in producing

20   commercially important proteins such as enzymes used in amino acid biosynthesis, metabolism, transcription, translation, RNA processing, nucleic acid and a protein degradation, protein modification and DNA replication, restriction, modification, recombination and repair.

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The present invention further provides systems, particularly computer-based systems, which contain the sequence information described herein. Such systems are designed to identify commercially important fragments of the nucleic acid molecule of the present invention. As used herein, "a computer-based system" refers to the hardware means, software means and data storage means used to analyze the nucleotide sequence information of the present invention. The minimum hardware means of the computer-based systems of the present invention comprises a central processing unit (CPU), input means, output means and data storage means. A skilled artisan can readily appreciate that any one of the currently available computer-based system are suitable for use in the present invention.

As indicated above, the computer-based systems of the present invention comprise a data storage means having stored therein a nucleotide sequence of the present invention and the necessary hardware means and software means for supporting and implementing a search means. As used herein, "data storage means" refers to memory that can store nucleotide sequence information of the present invention, or a memory access means which can access manufactures having recorded thereon the nucleotide sequence information of the present invention. As used herein, "search means" refers to one or more programs which are implemented on the computer-based system to compare a target sequence or target structural motif with the sequence information stored within the data storage means. Search means are used to identify fragments or regions of the sequence of the present invention that match a particular target sequence or target motif. A variety of known algorithms are disclosed publicly and a variety of commercially available software for conducting search means are available can be used in the computer-based systems of the present invention. Examples of such software include, but are not limited to, MacPattern (EMBL), BLASTIN and BLASTIX (NCBIA). One of the available algorithms or

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implementing software packages for conducting homology searches can be adapted for use in the present computer-based systems.

The most preferred sequence length of a target sequence is from about 10 to 100 amino acids or from about 30 to 300 nucleotide residues. However, it is well recognized that during searches for commercially important fragments of the nucleic acid molecules of the present invention, such as sequence fragments involved in gene expression and protein processing, may be of shorter length.

As used herein, "a target structural motif," or "target motif," refers to any rationally selected sequence or combination of sequences in which the sequences the sequence(s) are chosen based on a three-dimensional configuration which is formed upon the folding of the target motif. There are a variety of target motifs known in the art. Protein target motifs include, but are not limited to, enzymatic active sites and signal sequences. Nucleic acid target motifs include, but are not limited to, promoter sequences, *cis* elements, hairpin structures and inducible expression elements (protein binding sequences).

Thus, the present invention further provides an input means for receiving a target sequence, a data storage means for storing the target sequences of the present invention sequence identified using a search means as described above and an output means for outputting the identified homologous sequences. A variety of structural formats for the input and output means can be used to input and output information in the computer-based systems of the present invention. A preferred format for an output means ranks fragments of the sequence of the present invention by varying degrees of homology to the target sequence or target motif. Such presentation provides a skilled artisan with a ranking of sequences which contain various

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amounts of the target sequence or target motif and identifies the degree of homology contained in the identified fragment.

A variety of comparing means can be used to compare a target sequence or target motif with the data storage means to identify sequence fragments sequence of the present invention. For example, implementing software which implement the BLAST and BLAZE algorithms (Altschul *et al., J. Mol. Biol. 215*:403-410 (1990)) can be used to identify open frames within the nucleic acid molecules of the present invention. A skilled artisan can readily recognize that any one of the publicly available homology search programs can be used as the search means for the computer-based systems of the present invention.

Having now generally described the invention, the same will be more readily understood through reference to the following examples which are provided by way of illustration and are not intended to be limiting of the present invention, unless specified.

Example 1

The MONN01 cDNA library is a normalized library generated from maize (DK604, Dekalb Genetics, Dekalb, Illinois U.S.A.) total leaf tissue at the V6 plant development stage. Seeds are planted at a depth of approximately 3 cm into 2-3 inch peat pots containing Metro 200 growing medium. After 2-3 weeks growth they are transplanted into 10 inch pots containing the same growing medium. Plants are watered daily before transplantation and three times a week after transplantation. Peters 15-16-17 fertilizer is applied three times per week after transplanting at a strength of 150 ppm N. Two to three times during the lifetime of the plant, from transplanting to flowering, a total of 900 mg Fe is added to each pot. Maize plants are grown in a greenhouse in 15 hr day/9 hr night cycles. The daytime temperature is approximately 80°F and

the nighttime temperature is approximately 70°F. Supplemental lighting is provided by 1000 W

sodium vapor lamps. Tissue is collected when maize plants are at the 6-leaf development stage.

The older, more juvenile leaves, which are in a basal position, as well as the younger, more adult

leaves, which are more apical are cut at the base of the leaves. The leaves are then pooled and

5 immediately transferred to liquid nitrogen containers in which the pooled leaves are crushed.

The harvested tissue is then stored at −80°C until RNA preparation. The RNA is purified from

the stored tissue and the cDNA library is constructed as described in Example 2.

The SATMON001 cDNA library is generated from maize (B73, Illinois Foundation

Seeds, Champaign, Illinois U.S.A.) immature tassels at the V6 plant development stage. Seeds

10 are planted at a depth of approximately 3 cm into 2-3 inch peat pots containing Metro 200

growing medium. After 2-3 weeks growth they are transplanted into 10 inch pots containing the

same growing medium. Plants are watered daily before transplantation and three times a week

after transplantation. Peters 15-16-17 fertilizer is applied three times per week after transplanting

at a strength of 150 ppm N. Two to three times during the lifetime of the plant, from

15 transplanting to flowering, a total of 900 mg Fe is added to each pot. Maize plants are grown in a

greenhouse in 15 hr day/9 hr night cycles. The daytime temperature is approximately 80°F and

the nighttime temperature is approximately 70°F. Supplemental lighting is provided by 1000 W

sodium vapor lamps. Tassel tissue from maize plants is collected at the V6 stage. At that stage

the tassel is an immature tassel of about 2-3 cm in length. Tassels are removed and frozen in

20 liquid nitrogen. The harvested tissue is then stored at −80°C until RNA preparation. The RNA

is purified from the stored tissue and the cDNA library is constructed as described in Example 2.

The SATMON003 library is generated from maize (B73 x Mo17, Illinois Foundation Seeds, Champaign, Illinois U.S.A.) roots at the V6 developmental stage. Seeds are planted at a depth of approximately 3 cm into 2-3 inch peat pots containing Metro 200 growing medium. After 2-3 weeks growth, the seedlings are transplanted into 10 inch pots containing the Metro

5   200 growing medium. Plants are watered daily before transplantation and approximately 3 times a week after transplantation. Peters 15-16-17 fertilizer is applied approximately three times per week after transplanting at a concentration of 150 ppm N. Two to three times during the life time of the plant from transplanting to flowering a total of approximately 900 mg Fe is added to each pot. Maize plants are grown in a green house in approximately 15hr day/9hr night cycles.

10   The daytime temperature is approximately 80°F and the nighttime temperature is approximately 70°F. Supplemental lighting is provided by 1000 W sodium vapor lamps. Tissue is collected when the maize plant is at the 6 leaf development stage. The root system is cut from maize plant and washed with water to free it from the soil. The tissue is then immediately frozen in liquid nitrogen. The harvested tissue is then stored at −80°C until RNA preparation. The RNA is

15   purified from the stored tissue and the cDNA library is constructed as described in Example 2.

The SATMON004 cDNA library is generated from maize (B73 x Mo17, Illinois Foundation Seeds, Champaign, Illinois U.S.A.) total leaf tissue at the V6 plant development stage. Seeds are planted at a depth of approximately 3 cm into 2-3 inch peat pots containing Metro 200 growing medium. After 2-3 weeks growth they are transplanted into 10 inch pots

20   containing the same growing medium. Plants are watered daily before transplantation and three times a week after transplantation. Peters 15-16-17 fertilizer is applied three times per week after transplanting at a strength of 150 ppm N. Two to three times during the lifetime of the plant,

from transplanting to flowering, a total of 900 mg Fe is added to each pot. Maize plants are grown in a greenhouse in 15 hr day/9 hr night cycles. The daytime temperature is approximately 80°F and the nighttime temperature is approximately 70°F. Supplemental lighting is provided by 1000 W sodium vapor lamps. Tissue is collected when the maize plant is at the 6-leaf

5   development stage. The older, more juvenile leaves, which are in a basal position, as well as the younger, more adult leaves, which are more apical are cut at the base of the leaves. The leaves are then pooled and immediately transferred to liquid nitrogen containers in which the pooled leaves are crushed. The harvested tissue is then stored at −80°C until RNA preparation. The RNA is purified from the stored tissue and the cDNA library is constructed as described in

10   Example 2.

The SATMON005 cDNA library is generated from maize (B73 x Mo17, Illinois Foundation Seeds, Champaign Illinois, U.S.A.) root tissue at the V6 development stage. Seeds are planted at a depth of approximately 3 cm into 2-3 inch peat pots containing Metro 200 growing medium. After 2-3 weeks growth they are transplanted into 10 inch pots containing the

15   same growing medium. Plants are watered daily before transplantation and three times a week after transplantation. Peters 15-16-17 fertilizer is applied three times per week after transplanting at a strength of 150 ppm N. Two to three times during the lifetime of the plant, from transplanting to flowering, a total of 900 mg Fe is added to each pot. Maize plants are grown in a green house in 15 hr day/9 hr night cycles. The daytime temperature is approximately 80°F and

20   the nighttime temperature is approximately 70°F. Supplemental lighting is provided by 1000 W sodium vapor lamps. Tissue is collected when the maize plant is at the 6-leaf development stage. The root system is cut from the mature maize plant and washed with water to free it from the

soil. The tissue is immediately frozen in liquid nitrogen and the harvested tissue is then stored at −80°C until RNA preparation. The RNA is purified from the stored tissue and the cDNA library is constructed as described in Example 2.

The SATMON006 cDNA library is generated from maize (B73 x Mo17, Illinois

5   Foundation Seeds, Champaign Illinois, U.S.A.) total leaf tissue at the V6 plant development stage. Seeds are planted at a depth of approximately 3 cm into 2-3 inch peat pots containing Metro 200 growing medium. After 2-3 weeks growth they are transplanted into 10 inch pots containing the same growing medium. Plants are watered daily before transplantation and three times a week after transplantation. Peters 15-16-17 fertilizer is applied three times per week after

10   transplanting at a strength of 150 ppm N. Two to three times during the lifetime of the plant, from transplanting to flowering, a total of 900 mg Fe is added to each pot. Maize plants are grown in a greenhouse in 15 hr day/9 hr night cycles. The daytime temperature is approximately 80°F and the nighttime temperature is approximately 70°F. Supplemental lighting is provided by 1000 W sodium vapor lamps. Tissue is collected when the maize plant is at the 6-leaf

15   development stage. The older more juvenile leaves, which are in a basal position, as well as the younger more adult leaves, which are more apical are cut at the base of the leaves. The leaves are then pooled and immediately transferred to liquid nitrogen containers in which the pooled leaves are crushed. The harvested tissue is then stored at −80°C until RNA preparation. The RNA is purified from the stored tissue and the cDNA library is constructed as described in

20   Example 2.

The SATMON007 cDNA library is generated from the primary root tissue of 5 day old maize (DK604, Dekalb Genetics, Dekalb, Illinois U.S.A.) seedlings. Seeds are planted on a

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moist filter paper on a covered tray that is kept in the dark until germination (one day). After

germination, the trays, along with the moist paper, are moved to a greenhouse where the maize

plants are grown in the greenhouse in 15 hr day/9 hr night cycles for approximately 5 days. The

daytime temperature is approximately 80°F and the nighttime temperature is approximately

5   70°F. Supplemental lighting is provided by 1000 W sodium vapor lamps. The primary root

tissue is collected when the seedlings are 5 days old. At this stage, the primary root (radicle) is

pushed through the coleorhiza which itself is pushed through the seed coat. The primary root,

which is about 2-3 cm long, is cut and immediately frozen in liquid nitrogen and then stored at –

80°C until RNA preparation. The RNA is purified from the stored tissue and the cDNA library

10   is constructed as described in Example 2.

The SATMON008 cDNA library is generated from the primary shoot (coleoptile 2-3 cm)

of maize (DK604, Dekalb Genetics, Dekalb, Illinois U.S.A.) seedlings which are approximately

5 days old. Seeds are planted on a moist filter paper on a covered tray that is kept in the dark

until germination (one day). Then the trays containing the seeds are moved to a greenhouse at

15   15hr daytime/9 hr nighttime cycles and grown until they are 5 days post germination. The

daytime temperature is approximately 80°F and the nighttime temperature is approximately

70°F. Tissue is collected when the seedlings are 5 days old. At this stage, the primary shoot

(coleoptile) is pushed through the seed coat and is about 2-3 cm long. The coleoptile is dissected

away from the rest of the seedling, immediately frozen in liquid nitrogen and then stored at

20   –80°C until RNA preparation. The RNA is purified from the stored tissue and the cDNA library

is constructed as described in Example 2.

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The SATMON009 cDNA library is generated from maize (DK604, Dekalb Genetics, Dekalb, Illinois U.S.A.) leaves at the 8 leaf stage (V8 plant development stage). Seeds are planted at a depth of approximately 3 cm into 2-3 inch peat pots containing Metro 200 growing medium. After 2-3 weeks growth they are transplanted into 10 inch pots containing the same

5   growing medium. Plants are watered daily before transplantation and three times a week after transplantation. Peters 15-16-17 fertilizer is applied three times per week after transplanting at a strength of 150 ppm N. Two to three times during the lifetime of the plant, from transplanting to flowering, a total of 900 mg Fe is added to each pot. Maize plants are grown in a green house in 15 hr day/9 hr night cycles. The daytime temperature is 80°F and the nighttime temperature is

10   70°F. Supplemental lighting is provided by 1000 W sodium vapor lamps. Tissue is collected when the maize plant is at the 8-leaf development stage. The older more juvenile leaves, which are in a basal position, as well as the younger more adult leaves, which are more apical, are cut at the base of the leaves. The leaves are then pooled and then immediately transferred to liquid nitrogen containers in which the pooled leaves are crushed. The harvested tissue is then stored at

15   −80°C until RNA preparation. The RNA is purified from the stored tissue and the cDNA library is constructed as described in Example 2.

The SATMON010 cDNA library is generated from maize (DK604, Dekalb Genetics, Dekalb, Illinois U.S.A.) root tissue at the V8 plant development stage. Seeds are planted at a depth of approximately 3 cm into 2-3 inch peat pots containing Metro 200 growing medium.

20   After 2-3 weeks growth they are transplanted into 10 inch pots containing the same growing medium. Plants are watered daily before transplantation and three times a week after transplantation. Peters 15-16-17 fertilizer is applied three times per week after transplanting at a

strength of 150 ppm N. Two to three times during the lifetime of the plant, from transplanting to flowering, a total of 900 mg Fe is added to each pot. Maize plants are grown in a green house in 15 hr day/9 hr night cycles. The daytime temperature is 80°F and the nighttime temperature is 70°F. Supplemental lighting is provided by 1000 W sodium vapor lamps. Tissue is collected

5   when the maize plant is at the V8 development stage. The root system is cut from this mature maize plant and washed with water to free it from the soil. The tissue is immediately frozen in liquid nitrogen. The harvested tissue is then stored at –80°C until RNA preparation. The RNA is purified from the stored tissue and the cDNA library is constructed as described in Example 2.

The SATMON011 cDNA library is generated from undeveloped maize (DK604, Dekalb

10   Genetics, Dekalb, Illinois U.S.A.) leaf at the V6 plant development stage. Seeds are planted at a depth of approximately 3 cm into 2-3 inch peat pots containing Metro 200 growing medium. After 2-3 weeks growth they are transplanted into 10 inch pots containing the same growing medium. Plants are watered daily before transplantation and three times a week after transplantation. Peters 15-16-17 fertilizer is applied three times per week after transplanting at a

15   strength of 150 ppm N. Two to three times during the lifetime of the plant, from transplanting to flowering, a total of 900 mg Fe is added to each pot. Maize plants are grown in a green house in 15 hr day/9 hr night cycles. The daytime temperature is approximately 80°F and the nighttime temperature is approximately 70°F. Supplemental lighting is provided by 1000 W sodium vapor lamps. Tissue is collected when the maize plant is at the 6-leaf development stage. The second

20   youngest leaf which is at the base of the apical leaf of V6 stage maize plant is cut at the base and immediately transferred to liquid nitrogen containers in which the leaf is crushed. The harvested

tissue is then stored at −80°C until RNA preparation. The RNA is purified from the stored tissue and the cDNA library is constructed as described in Example 2.

The SATMON012 cDNA library is generated from 2 day post germination maize (DK604, Dekalb Genetics, Dekalb, Illinois U.S.A.) seedlings. Seeds are planted on a moist filter paper on a covered tray that is kept in the dark until germination (one day). Then the trays containing the seeds are moved to the greenhouse and grown at 15hr daytime/9 hr nighttime cycles until 2 days post germination. The daytime temperature is approximately 80°F and the nighttime temperature is approximately 70°F. Tissue is collected when the seedlings are 2 days old. At the two day stage, the coleorhiza is pushed through the seed coat and the primary root (the radicle) is pierced the coleorhiza but is barely visible. Also, at this two day stage, the coleoptile is just emerging from the seed coat. The 2 days post germination seedlings are then immersed in liquid nitrogen and crushed. The harvested tissue is stored at −80°C until preparation of total RNA. The RNA is purified from the stored tissue and the cDNA library is constructed as described in Example 2.

The SATMON013 cDNA library is generated from apical maize (DK604, Dekalb Genetics, Dekalb, Illinois U.S.A.) meristem founder at the V4 plant development stage. Seeds are planted at a depth of approximately 3 cm into 2-3 inch peat pots containing Metro 200 growing medium. After 2-3 weeks growth they are transplanted into 10 inch pots containing the same growing medium. Plants are watered daily before transplantation and three times a week after transplantation. Peters 15-16-17 fertilizer is applied three times per week after transplanting at a strength of 150 ppm N. Two to three times during the lifetime of the plant, from transplanting to flowering, a total of 900 mg Fe is added to each pot. Maize plants are grown in a

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greenhouse in 15 hr day/9 hr night cycles. The daytime temperature is approximately 80°F and

the nighttime temperature is approximately 70°F. Supplemental lighting is provided by 1000 W

sodium vapor lamps. Prior to tissue collection, the plant is at the 4 leaf stage. The lead at the

apex of the V4 stage maize plant is referred to as the meristem founder. This apical meristem

5   founder is cut, immediately frozen in liquid nitrogen and crushed. The harvested tissue is then

stored at −80°C until RNA preparation. The RNA is purified from the stored tissue and the

cDNA library is constructed as described in Example 2.

The SATMON014 cDNA library is generated from maize (DK604, Dekalb Genetics,

Dekalb, Illinois U.S.A.) endosperm at fourteen days after pollination. Seeds are planted at a

10   depth of approximately 3 cm into 2-3 inch peat pots containing Metro 200 growing medium.

After 2-3 weeks growth they are transplanted into 10 inch pots containing the same growing

medium. Plants are watered daily before transplantation and three times a week after

transplantation. Peters 15-16-17 fertilizer is applied three times per week after transplanting at a

strength of 150 ppm N. Two to three times during the lifetime of the plant, from transplanting to

15   flowering, a total of 900 mg Fe is added to each pot. Maize plants are grown in a greenhouse in

15 hr day/9 hr night cycles. The daytime temperature is approximately 80°F and the nighttime

temperature is approximately 70°F. Supplemental lighting is provided by 1000 W sodium vapor

lamps. After the V10 stage, ear shoots are ready for fertilization. At this stage, the ear shoots are

enclosed in a paper bag before silk emergence to withhold the pollen. The ear shoots are

20   pollinated and 14 days after pollination, the ears are pulled out and then the kernels are plucked

out of the ears. Each kernel is then dissected into the embryo and the endosperm and the

aleurone layer is removed. After dissection, the endosperms are immediately frozen in liquid

nitrogen and then stored at −80°C until RNA preparation. The RNA is purified from the stored

tissue and the cDNA library is constructed as described in Example 2.

The SATMON016 cDNA library is generated from maize (DK604, Dekalb Genetics,

Dekalb, Illinois U.S.A.) sheath tissue collected at the V8 developmental stage. Seeds are planted

in a depth of approximately 3 cm in solid into 2-3 inch pots containing Metro growing medium.

After 2-3 weeks growth, they are transplanted into 10" pots containing the same. Plants are

watered daily before transplantation and approximately the times a week after transplantation.

Peters 15-16-17 fertilizer is applied approximately three times per week after transplanting, at a

strength of 150 ppm N. Two to three times during the life time of the plant from transplanting to

flowering, a total of approximately 900 mg Fe is added to each pot. Maize plants are grown in a

greenhouse in 15hr day/9hr night cycles. The daytime temperature is approximately 80°F and

the nighttime temperature is approximately 70°F. Supplemental lighting is provided by 1000 W

sodium vapor lamps. When the maize plants are at the V8 stage the 5th and 6th leaves from the

bottom exhibit fully developed leaf blades. At the base of these leaves, the ligule is

differentiated and the leaf blade is joined to the sheath. The sheath is dissected away from the

base of the leaf then the sheath is frozen in liquid nitrogen and crushed. The tissue is then stored

at −80°C until RNA preparation. The RNA is purified from the stored tissue and the cDNA

library is constructed as described in Example 2.

The SATMON017 cDNA library is generated from maize (DK604, Dekalb Genetics,

Dekalb, Illinois U.S.A.) embryo collected from plants at twenty one days after pollination. Seeds

are planted at a depth of approximately 3 cm into 2-3 inch peat pots containing Metro 200

growing medium. After 2-3 weeks growth the seeds are transplanted into 10 inch pots containing

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the same growing medium. Plants are watered daily before transplantation and three times a week after transplantation. Peters 15-16-17 fertilizer is applied three times per week after transplanting at a strength of 150 ppm N. Two to three times during the lifetime of the plant, from transplanting to flowering, a total of 900 mg Fe is added to each pot. Maize plants are

5   grown in a green house in 15 hr day/9 hr night cycles. The daytime temperature is approximately 80°F and the nighttime temperature is approximately 70°F. Supplemental lighting is provided by 1000 W sodium vapor lamps. After the V10 stage, the ear shoots of maize plant, which are ready for fertilization, are enclosed in a paper bag before silk emergence to withhold the pollen. The ear shoots are fertilized and 21 days after pollination, the ears are pulled out and the kernels are

10   plucked out of the ears. Each kernel is then dissected into the embryo and the endosperm and the aleurone layer is removed. After dissection, the embryos are immediately frozen in liquid nitrogen and then stored at –80°C until RNA preparation. The RNA is purified from the stored tissue and the cDNA library is constructed as described in Example 2.

The SATMON019 cDNA library is generated from maize (DK604, Dekalb Genetics,

15   Dekalb, Illinois U.S.A.) culm (stem) at the V8 developmental stage. Seeds are planted at a depth of approximately 3 cm into 2-3 inch peat pots containing Metro 200 growing medium. After 2-3 weeks growth they are transplanted into 10 inch pots containing the same growing medium. Plants are watered daily before transplantation and three times a week after transplantation. Peters 15-16-17 fertilizer is applied three times per week after transplanting at a strength of 150

20   ppm N. Two to three times during the lifetime of the plant, from transplanting to flowering, a total of 900 mg Fe is added to each pot. Maize plants are grown in a greenhouse in 15 hr day/9 hr night cycles. The daytime temperature is approximately 80°F and the nighttime temperature is

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approximately 70°F. Supplemental lighting is provided by 1000 W sodium vapor lamps. When the maize plant is at the V8 stage, the 5th and 6th leaves from the bottom have fully developed leaf blades. The region between the nodes of the 5th and the sixth leaves from the bottom is the region of the stem that is collected. The leaves are pulled out and the sheath is also torn away from the stem. This stem tissue is completely free of any leaf and sheath tissue. The stem tissue is then frozen in liquid nitrogen and stored at −80°C until RNA preparation. The RNA is purified from the stored tissue and the cDNA library is constructed as described in Example 2.

The SATMON020 cDNA library is from a maize (DK604, Dekalb Genetics, Dekalb, Illinois U.S.A.) Hill Type II-Initiated Callus. Petri plates containing approximately 25 ml of Type II initiation media are prepared. This medium contains N6 salts and vitamins, 3% sucrose, 2.3 g/liter proline 0.1 g/liter enzymatic casein hydrolysate, 2mg/liter 2,4 – dichloro phenoxy-acetic acid (2,4, D), 15.3 mg/liter $AgNO_3$ and 0.8% bacto agar and is adjusted to pH 6.0 before autoclaving. At 9-11 days after pollination, an ear with immature embryos measuring approximately 1-2 mm in length is chosen. The husks and silks are removed and then the ear is broken into halves and placed in an autoclaved solution of Clorox/TWEEN 20 sterilizing solution. Then the ear is rinsed with deionized water. Then each embryo is extracted from the kernel. Intact embryos are placed in contact with the medium, scutellar side up). Multiple embryos are plated on each plate and the plates are incubated in the dark at 25°C. Type II calluses are friable, can be subcultured with a spatula, frequently regenerate via somatic embryogenesis and are relatively undifferentiated. As seen in the microscope, the Tape II calluses show color ranging from translucent to light yellow and heterogeneity on with respect to embryoid structure as well as stage of embryoid development. Once Type II callus are formed,

the calluses is transferred to type II callus maintenance medium without $AgNO_3$. Every 7-10 days, the callus is subcultured. About 4 weeks after embryo isolation the callus is removed from the plates and then frozen in liquid nitrogen. The harvested tissue is stored at $-80°C$ until RNA preparation. The RNA is purified from the stored tissue and the cDNA library is constructed as described in Example 2.

The SATMON021 cDNA library is generated from the immature maize (DK604, Dekalb Genetics, Dekalb Illinois, U.S.A.) tassel at the V8 plant development stage. Seeds are planted at a depth of approximately 3 cm into 2-3 inch peat pots containing Metro 200 growing medium. After 2-3 weeks growth they are transplanted into 10 inch pots containing the same growing medium. Plants are watered daily before transplantation and three times a week after transplantation. Peters 15-16-17 fertilizer is applied three times per week after transplanting at a strength of 150 ppm N. Two to three times during the lifetime of the plant, from transplanting to flowering, a total of 900 mg Fe is added to each pot. Maize plants are grown in a greenhouse in 15 hr day/9 hr night cycles. The daytime temperature is approximately 80°F and the nighttime temperature is approximately 70°F. Supplemental lighting is provided by 1000 W sodium vapor lamps. As the maize plant enters the V8 stage, tassels which are 15-20 cm in length are collected and frozen in liquid nitrogen. The harvested tissue is stored at $-80°C$ until RNA preparation. The RNA is purified from the stored tissue and the cDNA library is constructed as described in Example 2.

The SATMON022 cDNA library is generated from maize (DK604, Dekalb Genetics, Dekalb, Illinois U.S.A.) immature ear at the V8 plant development stage. Seeds are planted at a depth of approximately 3 cm into 2-3 inch peat pots containing Metro 200 growing medium.

After 2-3 weeks growth they are transplanted into 10 inch pots containing the same growing medium. Plants are watered daily before transplantation and three times a week after transplantation. Peters 15-16-17 fertilizer is applied three times per week after transplanting at a strength of 150 ppm N. Two to three times during the lifetime of the plant, from transplanting to flowering, a total of 900 mg Fe is added to each pot. Maize plants are grown in a greenhouse in 15 hr day/9 hr night cycles. The daytime temperature is approximately 80°F and the nighttime temperature is approximately 70°F. Supplemental lighting is provided by 1000 W sodium vapor lamps. Tissue is collected when the plant is in the V8 stage. At this stage, some immature ear shoots are visible. The immature ear shoots (approximately 3-4 cm in length) are pulled out, frozen in liquid nitrogen and then stored at −80°C until RNA preparation. The RNA is purified from the stored tissue and the cDNA library is constructed as described in Example 2.

The SATMON023 cDNA library is generated from maize (DK604, Dekalb Genetics, Dekalb, Illinois U.S.A.) ear (growing silk) at the V8 development stage. Seeds are planted at a depth of approximately 3 cm into 2-3 inch peat pots containing Metro 200 growing medium. After 2-3 weeks growth they are transplanted into 10 inch pots containing the same growing medium. Plants are watered daily before transplantation and three times a week after transplantation. Peters 15-16-17 fertilizer is applied three times per week after transplanting at a strength of 150 ppm N. Two to three times during the lifetime of the plant, from transplanting to flowering, a total of 900 mg Fe is added to each pot. Maize plants are grown in a greenhouse in 15 hr day/9 hr night cycles. The daytime temperature is approximately 80°F and the nighttime temperature is approximately 70°F. When the tissue is harvested at the V8 stage, the length of the ear that is harvested is about 10-15 cm and the silks are just exposed (approximately 1 inch).

The ear along with the silks is frozen in liquid nitrogen and then the tissue is stored at −80°C until RNA preparation. The RNA is purified from the stored tissue and the cDNA library is constructed as described in Example 2.

The SATMON024 cDNA library is generated from the immature maize (DK604, Dekalb Genetics, Dekalb, Illinois U.S.A.) tassel at the V9 development stage. Seeds are planted at a depth of approximately 3 cm into 2-3 inch peat pots containing Metro 200 growing medium. After 2-3 weeks growth they are transplanted into 10 inch pots containing the same growing medium. Plants are watered daily before transplantation and three times a week after transplantation. Peters 15-16-17 fertilizer is applied three times per week after transplanting at a strength of 150 ppm N. Two to three times during the lifetime of the plant, from transplanting to flowering, a total of 900 mg Fe is added to each pot. Maize plants are grown in a greenhouse in 15 hr day/9 hr night cycles. The daytime temperature is approximately 80°F and the nighttime temperature is approximately 70°F. As a maize plant enters the V9 stage, the tassel is rapidly developing and a 37 cm tassel along with the glume, anthers and pollen is collected and frozen in liquid nitrogen. The harvested tissue is stored at −80°C until RNA preparation. The RNA is purified from the stored tissue and the cDNA library is constructed as described in Example 2.

The SATMON025 cDNA library is from maize (DK604, Dekalb Genetics, Dekalb, Illinois U.S.A.) Hill Type II-Regenerated Callus. Type II callus is grown in initiation media as described for SATMON020 and then the embryoids on the surface of the Type II callus are allowed to mature and germinate. The 1-2 gm fresh weight of the soft friable type callus containing numerous embryoids are transferred to 100 x 15 mm petri plates containing 25 ml of regeneration media. Regeneration media consists of Murashige and Skoog (MS) basal salts,

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modified White's vitamins (0.2 g/liter glycine and 0.5 g/liter myo-inositoland 0.8% bacto agar (6SMS0D)). The plates are then placed in the dark after covering with parafilm. After 1 week, the plates are moved to a lighted growth chamber with 16 hr light and 8 hr dark photoperiod. Three weeks after plating the Type II callus to 6SMS0D, the callus exhibit shoot formation. The

5 callus and the shoots are transferred to fresh 6SMS0D plates for another 2 weeks. The callus and the shoots are then transferred to petri plates with reduced sucrose (3SMSOD). Upon distinct formation of a root and shoot, the newly developed green plants are then removed out with a spatula and frozen in liquid nitrogen containers. The harvested tissue is then stored at −80°C until RNA preparation. The RNA is purified from the stored tissue and the cDNA library is

10 constructed as described in Example 2.

The SATMON026 cDNA library is generated from maize (DK604, Dekalb Genetics, Dekalb, Illinois U.S.A.) juvenile/adult shift leaves at the V8 plant development stage. Seeds are planted at a depth of approximately 3 cm into 2-3 inch peat pots containing Metro 200 growing medium. After 2-3 weeks growth they are transplanted into 10 inch pots containing the same

15 growing medium. Plants are watered daily before transplantation and three times a week after transplantation. Peters 15-16-17 fertilizer is applied three times per week after transplanting at a strength of 150 ppm N. Two to three times during the lifetime of the plant, from transplanting to flowering, a total of 900 mg Fe is added to each pot. Maize plants are grown in a greenhouse in 15 hr day/9 hr night cycles. The daytime temperature is approximately 80°F and the nighttime

20 temperature is approximately 70°F. Supplemental lighting is provided by 1000 W sodium vapor lamps. Tissue is collected when the maize plants are at the 8-leaf development stage. Leaves are founded sequentially around the meristem over weeks of time and the older, more juvenile leaves

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arise earlier and in a more basal position than the younger, more adult leaves, which are in a more apical position. In a V8 plant, some leaves which are in the middle portion of the plant exhibit characteristics of both juvenile as well as adult leaves. They exhibit a yellowing color but also exhibit, in part, a green color. These leaves are termed juvenile/adult shift leaves. The juvenile/adult shift leaves (the 4th, 5th leaves from the bottom) are cut at the base, pooled and transferred to liquid nitrogen in which they are then crushed. The harvested tissue is then stored at −80°C until RNA preparation. The RNA is purified from the stored tissue and the cDNA library is constructed as described in Example 2.

The SATMON027 cDNA library is generated from maize (DK604, Dekalb Genetics, Dekalb, Illinois U.S.A.) leaves from plants at the V8 developmental stage that are subject to six days water stress. Seeds are planted at a depth of approximately 3 cm into 2-3 inch peat pots containing Metro 200 growing medium. After 2-3 weeks growth they are transplanted into 10 inch pots containing the Metro 200 growing medium. Plants are watered daily before transplantation and three times a week after transplantation. Peters 15-16-17 fertilizer is applied three times per week after transplanting at a strength of 150 ppm N. Two to three times during the lifetime of the plant, from transplanting to flowering, a total of 900 mg Fe is added to each pot. Maize plants are grown in a greenhouse in 15 hr day/9 hr night cycles. The daytime temperature is approximately 80°F and the nighttime temperature is approximately 70°F. Supplemental lighting is provided by 1000 W sodium vapor lamps. Prior to tissue collection, when the plant is at the 8-leaf stage, water is held back for six days. The older, more juvenile leaves, which are in a basal position, as well as the younger, more adult leaves, which are more apical, are all cut at the base of the leaves. All the leaves exhibit significant wilting. The leaves

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are then pooled and immediately transferred to liquid nitrogen containers in which the pooled

leaves are then crushed. The harvested tissue is then stored at −80°C until RNA preparation.

The RNA is purified from the stored tissue and the cDNA library is constructed as described in

Example 2.

5   The SATMON028 cDNA library is generated from maize (DK604, Dekalb Genetics,

Dekalb, Illinois U.S.A.) roots at the V8 developmental stage that are subject to six days water

stress. Seeds are planted at a depth of approximately 3 cm into 2-3 inch peat pots containing

Metro 200 growing medium. After 2-3 weeks growth they are transplanted into 10 inch pots

containing the Metro 200 growing medium. Plants are watered daily before transplantation and

10   three times a week after transplantation. Peters 15-16-17 fertilizer is applied three times per

week after transplanting at a strength of 150 ppm N. Two to three times during the lifetime of

the plant, from transplanting to flowering, a total of 900 mg Fe is added to each pot. Maize

plants are grown in a greenhouse in 15 hr day/9 hr night cycles. The daytime temperature is

approximately 80°F and the nighttime temperature is approximately 70°F. Supplemental

15   lighting is provided by 1000 W sodium vapor lamps. Prior to tissue collection, when the plant is

at the 8-leaf stage, water is held back for six days. The root system is cut, shaken and washed to

remove soil. Root tissue is then pooled and immediately transferred to liquid nitrogen containers

in which the pooled leaves are then crushed. The harvested tissue is then stored at −80°C until

RNA preparation. The RNA is purified from the stored tissue and the cDNA library is

20   constructed as described in Example 2.

The SATMON029 cDNA library is generated from maize (DK604, Dekalb Genetics,

Dekalb, Illinois U.S.A.) seedlings at the etiolated stage. Seeds are planted on a moist filter paper

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on a covered tray that is kept in the dark for 4 days at approximately 70°F. Tissue is collected when the seedlings are 4 days old. By 4 days, the primary root has penetrated the coleorhiza and is about 4-5 cm and the secondary lateral roots have also made their appearance. The coleoptile has also pushed through the seed coat and is about 4-5 cm long. The seedlings are frozen in

5   liquid nitrogen and crushed. The RNA is purified from the stored tissue and the cDNA library is constructed as described in Example 2.

The SATMON030 cDNA library is generated from maize (DK604, Dekalb Genetics, Dekalb, Illinois U.S.A.) root tissue at the V4 plant development stage. Seeds are planted at a depth of approximately 3 cm into 2-3 inch peat pots containing Metro 200 growing medium.

10   After 2-3 weeks growth, they are transplanted into 10 inch pots containing the same. Plants are watered daily before transplantation and approximately 3 times a week after transplantation. Peters 15-16-17 fertilizer is applied approximately three times per week after transplanting, at a strength of 150 ppm N. Two to three times during the life time of the plant, from transplanting to flowering, a total of approximately 900 mg Fe is added to each pot. Maize plants are grown in a

15   greenhouse in 15hr day/9hr night cycles. The daytime temperature is approximately 80°F and the nighttime temperature is approximately 70°F. Supplemental lighting is provided by 1000 sodium vapor lamps. Tissue is collected when the maize plant is at the 4 leaf development stage. The root system is cut from the mature maize plant and washed with water to free it from the soil. The tissue is then immediately frozen in liquid nitrogen. The harvested tissue is then stored

20   at −80°C until RNA preparation. The RNA is purified from the stored tissue and the cDNA library is constructed as described in Example 2.

The SATMON031 cDNA library is generated from the maize (DK604, Dekalb Genetics, Dekalb, Illinois U.S.A.) leaf tissue at the V4 plant development stage. Seeds are planted at a depth of approximately 3 cm into 2-3 inch peat pots containing Metro 200 growing medium. After 2-3 weeks growth they are transplanted into 10 inch pots containing the same growing medium. Plants are watered daily before transplantation and three times a week after transplantation. Peters 15-16-17 fertilizer is applied three times per week after transplanting at a strength of 150 ppm N. Two to three times during the lifetime of the plant, from transplanting to flowering, a total of 900 mg Fe is added to each pot. Maize plants are grown in a greenhouse in 15 hr day/9 hr night cycles. The daytime temperature is 80°F and the nighttime temperature is 70°F. Supplemental lighting is provided by 1000 W sodium vapor lamps. Tissue is collected when the maize plant is at the 4-leaf development stage. The third leaf from the bottom is cut at the base and immediately frozen in liquid nitrogen and crushed. The tissue is immediately frozen in liquid nitrogen. The harvested tissue is then stored at −80°C until RNA preparation. The RNA is purified from the stored tissue and the cDNA library is constructed as described in Example 2.

The SATMON033 cDNA library is generated from maize (DK604, Dekalb Genetics, Dekalb, Illinois U.S.A.) embryo tissue from plants at 13 days after pollination. Seeds are planted at a depth of approximately 3 cm into 2-3 inch peat pots containing Metro 200 growing medium. After 2-3 weeks growth they are transplanted into 10 inch pots containing the same growing medium. Plants are watered daily before transplantation and three times a week after transplantation. Peters 15-16-17 fertilizer is applied three times per week after transplanting at a strength of 150 ppm N. Two to three times during the lifetime of the plant, from transplanting to

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flowering, a total of 900 mg Fe is added to each pot. Maize plants are grown in a greenhouse in 15 hr day/9 hr night cycles. The daytime temperature is approximately 80°F and the nighttime temperature is approximately 70°F. Supplemental lighting is provided by 1000 W sodium vapor lamps. After the V10 stage, the ear shoots of the maize plant, which are ready for fertilization,

5   are enclosed in a paper bag before silk emergent to withhold the pollen. The ear shoots are pollinated and 13 days after pollination, the ears are pulled out and then the kernels are plucked cut of the ears. Each kernel is then dissected into the embryo and the endosperm and the aleurone layer is removed. After dissection, the embryos are immediately frozen in liquid nitrogen and then stored at −80°C until RNA preparation. The RNA is purified from the stored

10   tissue and the cDNA library is constructed as described in Example 2.

The SATMON034 cDNA library is generated from cold stressed maize (DK604, Dekalb Genetics, Dekalb, Illinois U.S.A.) seedlings. Seeds are planted on a moist filter paper on a covered tray that is kept on at 10°C for 7 days. After 7 days, the temperature is shifted to 15°C for one day until germination of the seed. Tissue is collected once the seedlings are 1 day old.

15   At this point, the coleorhiza has just pushed out of the seed coat and the primary root is just making its appearance. The coleoptile has not yet pushed completely through the seed coat and is also just making its appearance. These 1 day old cold stressed seedlings are frozen in liquid nitrogen and crushed. The harvested tissue is then stored at −80°C until RNA preparation. The RNA is purified from the stored tissue and the cDNA library is constructed as described in

20   Example 2.

The SATMONN01 cDNA library is a normalized library generated from maize (B73, Illinois Foundation Seeds, Champaign, Illinois U.S.A.) immature tassels at the V6 plant

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development stage normalized tissue. Seeds are planted at a depth of approximately 3 cm into 2-3 inch peat pots containing Metro 200 growing medium. After 2-3 weeks growth they are transplanted into 10 inch pots containing the same growing medium. Plants are watered daily before transplantation and three times a week after transplantation. Peters 15-16-17 fertilizer is

5   applied three times per week after transplanting at a strength of 150 ppm N. Two to three times during the lifetime of the plant, from transplanting to flowering, a total of 900 mg Fe is added to each pot. Maize plants are grown in a greenhouse in 15 hr day/9 hr night cycles. The daytime temperature is approximately 80°F and the nighttime temperature is approximately 70°F. Supplemental lighting is provided by 1000 W sodium vapor lamps. Tissue from the maize plant

10   is collected at the V6 stage. At that stage the tassel is an immature tassel of about 2-3 cm in length. The tassels are removed and frozen in liquid nitrogen. The harvested tissue is then stored at −80°C until RNA preparation. The RNA is purified from the stored tissue and the normalized cDNA library is constructed as described in Example 2.

        The SATMONN04 cDNA library is a normalized library generated from maize (B73 x

15   Mo17, Illinois Foundation Seeds, Champaign, Illinois U.S.A.) total leaf tissue at the V6 plant development stage. Seeds are planted at a depth of approximately 3 cm into 2-3 inch peat pots containing Metro 200 growing medium. After 2-3 weeks growth they are transplanted into 10 inch pots containing the same growing medium. Plants are watered daily before transplantation and three times a week after transplantation. Peters 15-16-17 fertilizer is applied three times per

20   week after transplanting at a strength of 150 ppm N. Two to three times during the lifetime of the plant, from transplanting to flowering, a total of 900 mg Fe is added to each pot. Maize plants are grown in a greenhouse in 15 hr day/9 hr night cycles. The daytime temperature is

approximately 80°F and the nighttime temperature is approximately 70°F. Supplemental

lighting is provided by 1000 W sodium vapor lamps. Tissue is collected when the maize plant is

at the 6-leaf development stage. The older, more juvenile leaves, which are in a basal position,

as well as the younger, more adult leaves, which are more apical are cut at the base of the leaves.

5   The leaves are then pooled and immediately transferred to liquid nitrogen containers in which the

pooled leaves are crushed. The harvested tissue is then stored at −80°C until RNA preparation.

The RNA is purified from the stored tissue and the normalized cDNA library is constructed as

described in Example 2.

The SATMONN05 cDNA library is a normalized library generated from maize (B73 x

10   Mo17, Illinois Foundation Seeds, Champaign Illinois, U.S.A.) root tissue at the V6 development

stage. Seeds are planted at a depth of approximately 3 cm into 2-3 inch peat pots containing

Metro 200 growing medium. After 2-3 weeks growth they are transplanted into 10 inch pots

containing the same growing medium. Plants are watered daily before transplantation and three

times a week after transplantation. Peters 15-16-17 fertilizer is applied three times per week after

15   transplanting at a strength of 150 ppm N. Two to three times during the lifetime of the plant,

from transplanting to flowering, a total of 900 mg Fe is added to each pot. Maize plants are

grown in a green house in 15 hr day/9 hr night cycles. The daytime temperature is approximately

80°F and the nighttime temperature is approximately 70°F. Supplemental lighting is provided by

1000 W sodium vapor lamps. Tissue is collected when the maize plant is at the 6-leaf

20   development stage. The root system is cut from the mature maize plant and washed with water

to free it from the soil. The tissue is immediately frozen in liquid nitrogen and the harvested

tissue is then stored at −80°C until RNA preparation. The RNA is purified from the stored tissue and the normalized cDNA library is constructed as described in Example 2.

The SATMONN06 cDNA library is a normalized library generated from maize (B73 x Mo17, Illinois Foundation Seeds, Champaign Illinois, U.S.A.) total leaf tissue at the V6 plant development stage. Seeds are planted at a depth of approximately 3 cm into 2-3 inch peat pots containing Metro 200 growing medium. After 2-3 weeks growth they are transplanted into 10 inch pots containing the same growing medium. Plants are watered daily before transplantation and three times a week after transplantation. Peters 15-16-17 fertilizer is applied three times per week after transplanting at a strength of 150 ppm N. Two to three times during the lifetime of the plant, from transplanting to flowering, a total of 900 mg Fe is added to each pot. Maize plants are grown in a greenhouse in 15 hr day/9 hr night cycles. The daytime temperature is approximately 80°F and the nighttime temperature is approximately 70°F. Supplemental lighting is provided by 1000 W sodium vapor lamps. Tissue is collected when the maize plant is at the 6-leaf development stage. The older more juvenile leaves, which are in a basal position, as well as the younger more adult leaves, which are more apical are cut at the base of the leaves. The leaves are then pooled and immediately transferred to liquid nitrogen containers in which the pooled leaves are crushed. The harvested tissue is then stored at −80°C until RNA preparation. The RNA is purified from the stored tissue and the normalized cDNA library is constructed as described in Example 2.

LIB36 is a normalized cDNA library prepared from maize (DK604, Dekalb Genetics, Dekalb, Illinois U.S.A) leaves harvested from V8 stage plants. Seeds are planted at a depth of approximately 3 cm in soil into 2"-3" peat pots containing Metro 200 growing medium. After 2-

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3 weeks growth, they are transplanted into 10" pots containing the same. Plants are watered daily before transplantation and three times a week after transplantation. Peters 15-16-17 fertilizer is applied three times per week after transplanting at a strength of 150 ppm N. Two to three times during the lifetime of the plant, from transplanting to flowering, a total of 900 mg Fe is added to each pot. Maize plants are grown in a green house in 15hr day /9hr night cycles. The daytime temperature is 80°F and the night time temperature is 70°F. Lighting is provided by 1000 W sodium vapor lamps. Tissue is collected from V8 stage plants. The older more juvenile leaves which are in a basal position as well as the younger more adult leaves which are more apical were all cut at the base of the leaves. The leaves are then pooled and then immediately transferred to liquid nitrogen containers in which the pooled leaves are then crushed. The harvested tissue is then stored at -80°C until RNA preparation.

For the construction of a cDNA library, the Superscript™ Plasmid System for cDNA synthesis and Plasmid Cloning (Gibco BRL, Life Technologies, Gaithersburg, MD) or similar system, following the conditions suggested by the manufacturer, is used. Poly A+ mRNA is purified from the total RNA preparation using Dynabeads® Oligo (dT)$_{25}$ (Dynal Inc., Lake Success, NY), or equivalent methods. Clones are selected and the plasmid DNA is isolated using a commercially available kit for normalizing the cDNA library.

LIB83 is a normalized cDNA library prepared from maize (DK604, Dekalb Genetics, Dekalb, Illinois U.S.A) leaves harvested from V8 stage plants. Seeds are planted at a depth of approximately 3 cm in soil into 2"-3" peat pots containing Metro 200 growing medium. After 2-3 weeks growth, they are transplanted into 10" pots containing the same. Plants are watered daily before transplantation and three times a week after transplantation. Peters 15-16-17 fertilizer is

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applied three times per week after transplanting at a strength of 150 ppm N. Two to three times

during the lifetime of the plant, from transplanting to flowering, a total of 900 mg Fe is added to

each pot. Plants are grown in a greenhouse in 15hr day /9hr night cycles. The daytime

temperature is 80°F and the night time temperature was 70°F. Lighting was provided by 1000 W

5   sodium vapor lamps. Tissue is collected from V8 stage plants. The older more juvenile leaves

which are in a basal position as well as the younger more adult leaves which are more apical

were all cut at the base of the leaves. The leaves are then pooled and then immediately

transferred to liquid nitrogen containers in which the pooled leaves are then crushed The

harvested tissue is then stored at -80°C until RNA preparation.

10   For the construction of a cDNA library, the Superscript™ Plasmid System for cDNA

synthesis and Plasmid Cloning (Gibco BRL, Life Technologies, Gaithersburg, MD) or similar

system, following the conditions suggested by the manufacturer, is used. Poly A+ mRNA is

purified from the total RNA preparation using Dynabeads® Oligo (dT)$_{25}$ (Dynal Inc., Lake

Success, NY), or equivalent methods. Clones are selected and the plasmid DNA is isolated using

15   a commercially available kit for normalizing the cDNA library.

LIB84 a normalized cDNA library is prepared from maize (DK604, Dekalb Genetics,

Dekalb, Illinois U.S.A) leaves harvested from V8 stage plants. Seeds are planted at a depth of

approximately 3 cm in soil into 2"-3" peat pots containing Metro 200 growing medium. After 2-

3 weeks growth, they are transplanted into 10" pots containing the same. Plants are watered

20   daily before transplantation and three times a week after transplantation. Peters 15-16-17

fertilizer is applied three times per week after transplanting at a strength of 150 ppm N. Two to

three times during the lifetime of the plant, from transplanting to flowering, a total of 900 mg Fe

is added to each pot. Plants were grown in a greenhouse in 15hr day /9hr night cycles. The daytime temperature was 80°F and the night time temperature was70 °F. Lighting was provided by 1000 W sodium vapor lamps. Tissue was collected from V8 stage plants. The older more juvenile leaves which are in a basal position as well as the younger more adult leaves which are

5   more apical were all cut at the base of the leaves. The leaves are then pooled and then immediately transferred to liquid nitrogen containers in which the pooled leaves are then crushed. The harvested tissue is then stored at -80°C until RNA preparation.

For the construction of a cDNA library, the Superscript™ Plasmid System for cDNA synthesis and Plasmid Cloning (Gibco BRL, Life Technologies, Gaithersburg, MD) or similar

10   system, following the conditions suggested by the manufacturer, is used. Poly A+ mRNA is purified from the total RNA preparation using Dynabeads® Oligo $(dT)_{25}$ (Dynal Inc., Lake Success, NY), or equivalent methods. Clones are selected and the plasmid DNA is isolated using a commercially available kit for normalizing the cDNA library.

The CMz029 (SATMON036) cDNA library is generated from maize (DK604, Dekalb

15   Genetics, Dekalb, Illinois U.S.A.) endosperm 22 days after pollination. Seeds are planted at a depth of approximately 3 cm into 2-3 inch peat pots containing Metro 200 growing medium. After 2-3 weeks growth they are transplanted into 10 inch pots containing the same growing medium. Plants are watered daily before transplantation and three times a week after transplantation. Peters 15-16-17 fertilizer is applied three times per week after transplanting at a

20   strength of 150 ppm N. Two to three times during the lifetime of the plant, from transplanting to flowering, a total of 900 mg Fe is added to each pot. Maize plants are grown in a greenhouse in 15 hr day/9 hr night cycles. The daytime temperature is approximately 80°F and the nighttime

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temperature is approximately 70°F. Supplemental lighting is provided by 1000 W sodium vapor lamps. After the V10 stage, the ear shoots of the maize plant, which are ready for fertilization, are enclosed in a paper bag before silk emergent to withhold the pollen. The ear shoots are pollinated and 22 days after pollination, the ears are pulled out and then the kernels are plucked

5 out of the ears. Each kernel is then dissected into the embryo and the endosperm and the alurone layer is removed. After dissection, the endosperms are immediately frozen in liquid nitrogen and then stored at −80°C until RNA preparation. The RNA is purified from the stored tissue and the cDNA library is constructed as described in Example 2.

The CMz030 (Lib143) cDNA library is generated from maize (DK604, Dekalb Genetics,

10 Dekalb, Illinois U.S.A.) seedling tissue two days post germination. Seeds are planted on a moist filter paper on a covered try that is keep in the dark until germination. The trays are then moved to the bench top at 15 hr daytime/9 hr nighttime cycles for 2 days post-germination. The day time temperature is 80°F and the nighttime temperature is 70°F. Tissue is collected when the seedlings are 2 days old. At this stage, the colehrhiza has pushed through the seed coat and the

15 primary root (the radicle) is just piercing the colehrhiza and is barely visible. The seedlings are placed at 42°C for 1 hour. Following the heat shock treatment, the seedlings are immersed in liquid nitrogen and crushed. The harvested tissue is stored at −80° until RNA preparation. The RNA is purified from the stored tissue and the cDNA library is constructed as described in Example 2.

20 The CMz031 (Lib148) cDNA library is generated from maize (DK604, Dekalb Genetics, Dekalb, Illinois U.S.A.) pollen tissue at the V10+ plant development stage. Seeds are planted at a depth of approximately 3 cm into 2-3 inch peat pots containing Metro 200 growing medium.

After 2-3 weeks growth they are transplanted into 10 inch pots containing the same growing medium. Plants are watered daily before transplantation and three times a week after transplantation. Peters 15-16-17 fertilizer is applied three times per week after transplanting at a strength of 150 ppm N. Two to three times during the lifetime of the plant, from transplanting to flowering, a total of 900 mg Fe is added to each pot. Maize plants are grown in a greenhouse in 15 hr day/9 hr night cycles. The daytime temperature is approximately 80°F and the nighttime temperature is approximately 70°F. Supplemental lighting is provided by 1000 W sodium vapor lamps. Tissue is collected from V10+ stage plants. The ear shoots, which are ready for fertilization, are enclosed in a paper bag to withhold pollen. Twenty-one days after pollination, prior to removing the ears, the paper bag is shaken to collect the mature pollen. The mature pollen is immediately frozen in liquid nitrogen containers and the pollen is crushed. The harvested tissue is then stored at −80°C until RNA preparation. The RNA is purified from the stored tissue and the cDNA library is constructed as described in Example 2.

The CMz033 (Lib189) cDNA library is generated from maize (RX601 Asgrow, Asgrow Seed Company, Des Moines, Iowa U.S.A.) pooled leaf tissue harvested from field grown plants at Asgrow research stations. Leaves are harvested at anthesis from open pollinated plants in a field (mulitple row) setting. The ear leaves from 10-12 plants are harvested, pooled, frozen in liquid nitrogen and then frozen at -80C where they are stored until RNA preparation. The RNA is purified from the stored tissue and the cDNA library is constructed as described in Example 2.

The CMz034 (Lib3060) cDNA library is generated from maize (DK604, Dekalb Genetics, Dekalb, Illinois U.S.A.) senescing leaves from plants at 40 days after pollination. Seeds are planted at a depth of approximately 3 cm into 2-3 inch peat pots containing Metro 200

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growing medium. After 2-3 weeks growth they are transplanted into 10 inch pots containing the same growing medium. Plants are watered daily before transplantation and three times a week after transplantation. Peters 15-16-17 fertilizer is applied three times per week after transplanting at a strength of 150 ppm N. Two to three times during the lifetime of the plant, from

5   transplanting to flowering, a total of 900 mg Fe is added to each pot. Maize plants are grown in a greenhouse in 15 hr day/9 hr night cycles. The daytime temperature is approximately 80°F and the nighttime temperature is approximately 70°F. Supplemental lighting is provided by 1000 W sodium vapor lamps. Tissue is collected from leaves located two leaves below the ear leaf. This sample represents those genes expressed during onset and early stages of leaf senescence. The

10   leaves are pooled and immediately transferred to liquid nitrogen. The harvested tissue is then stored at –80°C until RNA preparation. The RNA is purified from the stored tissue and the cDNA library is constructed as described in Example 2.

The CMz035 (Lib3061) cDNA library is generated from maize (DK604, Dekalb Genetics, Dekalb, Illinois U.S.A.) endosperm tissue from plants at 32 days after pollination.

15   Seeds are planted at a depth of approximately 3 cm into 2-3 inch peat pots containing Metro 200 growing medium. After 2-3 weeks growth they are transplanted into 10 inch pots containing the same growing medium. Plants are watered daily before transplantation and three times a week after transplantation. Peters 15-16-17 fertilizer is applied three times per week after transplanting at a strength of 150 ppm N. Two to three times during the lifetime of the plant, from

20   transplanting to flowering, a total of 900 mg Fe is added to each pot. Maize plants are grown in a greenhouse in 15 hr day/9 hr night cycles. The daytime temperature is approximately 80°Fand the nighttime temperature is approximately 70°F. Supplemental lighting is provided by 1000 W

sodium vapor lamps. Tissue is collected from V10+ stage plants. The ear shoots, which are ready for fertilization, are enclosed in a paper bag prior to silk emergence to withhold pollen. Thirty-two days after pollination, the ears are pulled out and the kernels are removed from the cob. Each kernel is dissected into the embryo and the endosperm and the aleurone layer is

5   removed. After dissection, the endosperms are immediately transferred to liquid nitrogen. The harvested tissue is then stored at 80°C until RNA preparation. The RNA is purified from the stored tissue and the cDNA library is constructed as described in Example 2.

The CMz036 (Lib3062) cDNA library is generated from maize (H99, USDA Maize Germplasm Collection, Urban, Illinois U.S.A.) husk tissue from 8 week old plants. Seeds are

10   planted at a depth of approximately 3 cm into 2-3 inch peat pots containing Metro 200 growing medium. After 2-3 weeks growth they are transplanted into 10 inch pots containing the same growing medium. Plants are watered daily before transplantation and three times a week after transplantation. Peters 15-16-17 fertilizer is applied three times per week after transplanting at a strength of 150 ppm N. Two to three times during the lifetime of the plant, from transplanting to

15   flowering, a total of 900 mg Fe is added to each pot. Maize plants are grown in a greenhouse in 15 hr day/9 hr night cycles. The daytime temperature is approximately 80°F and the nighttime temperature is approximately 70°F. Supplemental lighting is provided by 1000 W sodium vapor lamps. Tissue is collected from 8 week old plants. The husk is separated from the ear and immediately transferred to liquid nitrogen containers. The harvested tissue is then stored at

20   –80°C until RNA preparation. The RNA is purified from the stored tissue and the cDNA library is constructed as described in Example 2.

The CMz037 (Lib3059) cDNA library is generated from maize (RX601 Asgrow, Asgrow Seed Company, Des Moines, Iowa U.S.A) pooled kernels from plants at 12-15 days after pollination. Sample are collected from field grown material. Whole kernels from hand pollinated (control pollination) are harvested as whole ears and immediately frozen on dry ice.

5 Kernels from 10-12 ears are pooled and ground together in liquid nitrogen. The harvested tissue is then stored at –80°C until RNA preparation. The RNA is purified from the stored tissue and the cDNA library is constructed as described in Example 2.

The CMz039 (Lib3066) cDNA library is generated from maize (H99 USDA Maize Germplasm Collection, Urban, Illinois U.S.A.) immature anther tissue at the 7 week old immature tassel stage. Seeds are planted at a depth of approximately 3 cm into 2-3 inch peat pots

10 containing Metro 200 growing medium. After 2-3 weeks growth they are transplanted into 10 inch pots containing the same growing medium. Plants are watered daily before transplantation and three times a week after transplantation. Peters 15-16-17 fertilizer is applied three times per week after transplanting at a strength of 150 ppm N. Two to three times during the lifetime of

15 the plant, from transplanting to flowering, a total of 900 mg Fe is added to each pot. Maize plants are grown in a greenhouse in 15 hr day/9 hr night cycles. The daytime temperature is approximately 80°F and the nighttime temperature is approximately 70°F. Supplemental lighting is provided by 1000 W sodium vapor lamps. Tissue is collected when the maize plant is at the 7 week old immature tassel stage. At this stage, prior to anthesis, the immature anthers are

20 green and enclosed in the staminate spikelet. The developing anthers are dissected away from the 7 week old immature tassel and immediately frozen in liquid nitrogen. The harvested tissue

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is then stored at −80°C until RNA preparation. The RNA is purified from the stored tissue and the cDNA library is constructed as described in Example 2.

The CMz040 (Lib3067) cDNA library is generated from maize (MO17 USDA Maixe Germplasm Collection, Urbana, Illinois U.S.A.) kernel tissue from plants at the V10+ plant

5   development stage. Seeds are planted at a depth of approximately 3 cm into 2-3 inch peat pots containing Metro 200 growing medium. After 2-3 weeks growth they are transplanted into 10 inch pots containing the same growing medium. Plants are watered daily before transplantation and three times a week after transplantation. Peters 15-16-17 fertilizer is applied three times per week after transplanting at a strength of 150 ppm N. Two to three times during the lifetime of

10   the plant, from transplanting to flowering, a total of 900 mg Fe is added to each pot. Maize plants are grown in a greenhouse in 15 hr day/9 hr night cycles. The daytime temperature is approximately 80°F and the nighttime temperature is approximately 70°F. Supplemental lighting is provided by 1000 W sodium vapor lamps. Tissue is collected from V10+ stage plants. The ear shoots, which are ready for fertilization, are enclosed in a paper bag before silk

15   emergence to withhold pollen. Five to eight days after controlled pollination. The ears are pulled and the kernels removed. The kernels are immediately frozen in liquid nitrogen. This sample represents genes expressed in early kernel development, during periods of cell division, amyloplast biogenesis and early carbon flow across the material to filial tissue. The harvested kernels tissue is then stored at −80°C until RNA preparation. The RNA is purified from the

20   stored tissue and the cDNA library is constructed as described in Example 2.

The CMz041 (Lib3068) cDNA library is generated from maize pollen germinating silk tissue from plants at the V10+ plant development stage. Maize MO17 and H99 (USDA Maize

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Germplasm Collection, Urbana, Illinois U.S.A.) seeds are planted at a depth of approximately 3

cm into 2-3 inch peat pots containing Metro 200 growing medium. After 2-3 weeks growth they

are transplanted into 10 inch pots containing the same growing medium. Plants are watered daily

before transplantation and three times a week after transplantation. Peters 15-16-17 fertilizer is

5   applied three times per week after transplanting at a strength of 150 ppm N. Two to three times

during the lifetime of the plant, from transplanting to flowering, a total of 900 mg Fe is added to

each pot. Maize plants are grown in a greenhouse in 15 hr day/9 hr night cycles. The daytime

temperature is approximately 80°F and the nighttime temperature is approximately 70°F.

Supplemental lighting is provided by 1000 W sodium vapor lamps. Tissue is collected from

10   V10+ stage plants when the ear shoots are ready for fertilization at the silk emergence stage. The

H99 emerging silks are pollinated with an excess of MO17 pollen under controlled pollination

conditions in the green house. Eighteen hours after pollination the silks are removed from the

ears and immediately frozen in liquid nitrogen. This sample represents genes expressed in both

pollen and silk tissue early in pollination. The harvested tissue is then stored at −80°C until

15   RNA preparation. The RNA is purified from the stored tissue and the cDNA library is

constructed as described in Example 2.

The CMz042 (Lib3069) cDNA library is generated from maize ear tissue excessively

pollinated at the V10+ plant development stage. Maize MO17 and H99 (USDA Maize

Germplasm Collection, Urbana, Illinois U.S.A.) seeds are planted at a depth of approximately 3

20   cm into 2-3 inch peat pots containing Metro 200 growing medium. After 2-3 weeks growth they

are transplanted into 10 inch pots containing the same growing medium. Plants are watered daily

before transplantation and three times a week after transplantation. Peters 15-16-17 fertilizer is

applied three times per week after transplanting at a strength of 150 ppm N. Two to three times during the lifetime of the plant, from transplanting to flowering, a total of 900 mg Fe is added to each pot. Maize plants are grown in a greenhouse in 15 hr day/9 hr night cycles. The daytime temperature is approximately 80°F and the nighttime temperature is approximately 70°F.

5   Supplemental lighting is provided by 1000 W sodium vapor lamps. Tissue is collected from V10+ stage plants and the ear shoots which are ready for fertilization are at the silk emergence stage. The H99 immature ears are pollinated with an excess of MO17 pollen under controlled pollination conditions. Eighteen hours post-pollination, the ears are removed and immediately transferred to liquid nitrogen containers. The harvested tissue is then stored at −80°C until RNA

10   preparation. The RNA is purified from the stored tissue and the cDNA library is constructed as described in Example 2.

The CMz044 (Lib3075) cDNA library is generated from maize (H99, USDA Maize Germplasm Collection, Urbana, Illinois U.S.A.) microspore tissue from plants at the V10+ plant development stage. Seeds are planted at a depth of approximately 3 cm into 2-3 inch peat pots

15   containing Metro 200 growing medium. After 2-3 weeks growth they are transplanted into 10 inch pots containing the same growing medium. Plants are watered daily before transplantation and three times a week after transplantation. Peters 15-16-17 fertilizer is applied three times per week after transplanting at a strength of 150 ppm N. Two to three times during the lifetime of the plant, from transplanting to flowering, a total of 900 mg Fe is added to each pot. Maize

20   plants are grown in a greenhouse in 15 hr day/9 hr night cycles. The daytime temperature is approximately 80°F and the nighttime temperature is approximately 70°F. Supplemental lighting is provided by 1000 W sodium vapor lamps. Tissue is collected from immature anthers

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from 7 week old tassels. The immature anthers are first dissected from the 7 week old tassel with a scalpel on a glass slide covered with water. The microspores (immature pollen) are released into the water and are recovered by centrifugation. The microspore suspension is immediately frozen in liquid nitrogen. The harvested tissue is then stored at −80°C until RNA preparation.

5   The RNA is purified from the stored tissue and the cDNA library is constructed as described in Example 2.

The CMz045 (Lib3076) cDNA library is generated from maize (H99 USDA Maize Germplasm Collection, Urbana, Illinois U.S.A.) immature ear megaspore tissue. Seeds are planted at a depth of approximately 3 cm into 2-3 inch peat pots containing Metro 200 growing medium. After 2-3 weeks growth they are transplanted into 10 inch pots containing the same growing medium. Plants are watered daily before transplantation and three times a week after transplantation. Peters 15-16-17 fertilizer is applied three times per week after transplanting at a strength of 150 ppm N. Two to three times during the lifetime of the plant, from transplanting to flowering, a total of 900 mg Fe is added to each pot. Maize plants are grown in a greenhouse in 15 hr day/9 hr night cycles. The daytime temperature is approximately 80°F and the nighttime temperature is approximately 70°F. Supplemental lighting is provided by 1000 W sodium vapor lamps. The immature ears are harvested from the 7 week old plants and are approximately 2.5 to 3 cm in length. The kernels are removed from the cob immediately frozen in liquid nitrogen. The harvested tissue is then stored at −80°C until RNA preparation. The RNA is purified from

20   the stored tissue and the cDNA library is constructed as described in Example 2.

The CMz047 (Lib3078) cDNA library is generated from maize (RX601, Asgrow Seed Company, Des Moines, Iowa, U.S.A.) CO_2 treated high-exposure shoot tissue at the V10+ plant

development stage. RX601 maize seeds are sterilized for 1 minute with a 10% Clorox solution. The seeds are rolled in germination paper, and germinated in 0.5 mM calcium sulfate solution for two days at 30°C. The seedlings are planted at a depth of approximately 3 cm into 2-3 inch peat pots containing Metro 200 growing medium at a rate of 2-3 seedlings per pot. Twenty pots are

5 placed into a high CO_2 environment (approximately 1000 ppm CO_2). Twenty plants were grown under ambient greenhouse CO_2 (approximately 450 ppm CO_2). Plants are hand watered. Peters 20-20-20 fertilizer is also lightly applied. Maize plants are grown in a greenhouse in 15 hr day/9 hr night cycles. The daytime temperature is approximately 80°F and the nighttime temperature is approximately 70°F. Supplemental lighting is provided by 1000 W sodium vapor lamps. At ten

10 days post planting, the shoots from both atmosphere are frozen in liquid nitrogen and lightly ground. The roots are washed in deionized water to remove the support media and the tissue is immediately transferred to liquid nitrogen containers. The harvested tissue is then stored at −80°C until RNA preparation. The RNA is purified from the stored tissue and the cDNA library is constructed as described in Example 2.

15 The CMz048 (Lib3079) cDNA library is generated from maize (MO17USDA Maize Germplasm Collection, Urbana, Illinois U.S.A) basal endosperm transfer layer tissue. Seeds are planted at a depth of approximately 3 cm into 2-3 inch peat pots containing Metro 200 growing medium. After 2-3 weeks growth they are transplanted into 10 inch pots containing the same growing medium. Plants are watered daily before transplantation and three times a week after

20 transplantation. Peters 15-16-17 fertilizer is applied three times per week after transplanting at a strength of 150 ppm N. Two to three times during the lifetime of the plant, from transplanting to flowering, a total of 900 mg Fe is added to each pot. Maize plants are grown in a greenhouse in

15 hr day/9 hr night cycles. The daytime temperature is approximately 80°F and the nighttime temperature is approximately 70°F. Supplemental lighting is provided by 1000 W sodium vapor lamps. Tissue is collected from V10+ maize plants. The ear shoots, which are ready for fertilization, are enclosed in a paper bag prior to silk emergence, to withhold the pollen. Kernels are harvested at 12 days post-pollination and placed on wet ice for dissection. The kernels are cross sectioned laterally, dissecting just above the pedicel region, including 1-2 mm of the lower endosperm and the basal endosperm transfer region. The pedicel and lower endosperm region containing the basal endosperm transfer layer is pooled and immediately frozen in liquid nitrogen. The harvested tissue is then stored at −80°C until RNA preparation. The RNA is purified from the stored tissue and the cDNA library is constructed as described in Example 2.

The CMz049(Lib3088) cDNA library is generated from maize (H99, USDA Maize Germplasm Collection, Urbana, Illinois U.S.A) immature anther tissue from 8 weeks old plants. Seeds are planted at a depth of approximately 3 cm into 2-3 inch peat pots containing Metro 200 growing medium. After 2-3 weeks growth they are transplanted into 10 inch pots containing the same growing medium. Plants are watered daily before transplantation and three times a week after transplantation. Peters 15-16-17 fertilizer is applied three times per week after transplanting at a strength of 150 ppm N. Two to three times during the lifetime of the plant, from transplanting to flowering, a total of 900 mg Fe is added to each pot. Maize plants are grown in a greenhouse in 15 hr day/9 hr night cycles. The daytime temperature is approximately 80°F and the nighttime temperature is approximately 70°F. Supplemental lighting is provided by 1000 W sodium vapor lamps. Ears were harvested from 8 week old plants and were approximately 3.5-4.5 cm long. Kernels were dissected away from cob, frozen in liquid nitrogen and stored at -80C

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until preparation of RNA. The RNA is purified from the stored tissue and the cDNA library is constructed as described in Example 2.

The CMz050 (Lib3114) cDNA library is generated from silks from maize (B73, Illinois Foundation Seeds, Champaign, Illinois U.S.A.) plants at the V10+ plant development stage.

5 Seeds are planted at a depth of approximately 3 cm into 2-3 inch peat pots containing Metro 200 growing medium. After 2-3 weeks growth they are transplanted into 10 inch pots containing the same growing medium. Plants are watered daily before transplantation and three times a week after transplantation. Peters 15-16-17 fertilizer is applied three times per week after transplanting at a strength of 150 ppm N. Two to three times during the lifetime of the plant, from

10 transplanting to flowering, a total of 900 mg Fe is added to each pot. Maize plants are grown in a greenhouse in 15 hr day/9 hr night cycles. The daytime temperature is approximately 80°F and the nighttime temperature is approximately 70°F. Supplemental lighting is provided by 1000 W sodium vapor lamps. Tissue is collected when the maize plant is beyond the 10-leaf development stage and the ear shoots are approximately 15-20 cm in length. The ears are pulled

15 and silks are separated from the ears and immediately transferred to liquid nitrogen containers. The harvested tissue is then stored at −80°C until RNA preparation. The RNA is purified from the stored tissue and the cDNA library is constructed as described in Example 2.

The SOYMON001 cDNA library is generated from soybean cultivar Asgrow 3244 (Asgrow Seed Company, Des Moines, Iowa U.S.A.) total leaf tissue at the V4 plant development

20 stage. Leaf tissue from 38, field grown V4 stage plants is harvested from the 4th node. Leaf tissue is removed from the plants and immediately frozen in dry-ice. The harvested tissue is then

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stored at −80°C until RNA preparation. The RNA is purified from the stored tissue and the cDNA library is constructed as described in Example 2.

The SOYMON002 cDNA library is generated from soybean cultivar Asgrow 3244 (Asgrow Seed Company, Des Moines, Iowa U.S.A.) root tissue at the V4 plant development

5   stage. Root tissue from 76, field grown V4 stage plants is harvested. The root systems is cut from the soybean plant and washed with water to free it from the soil and immediately frozen in dry-ice. The harvested tissue is then stored at −80°C until RNA preparation. The RNA is purified from the stored tissue and the cDNA library is constructed as described in Example 2.

The SOYMON003 cDNA library is generated from soybean cultivar Asgrow 3244

10   (Asgrow Seed Company, Des Moines, Iowa U.S.A.) seedling hypocotyl axis tissue harvested 2 day post-imbibition. Seeds are planted at a depth of approximately 2cm into 2-3 inch peat pots containing Metromix 350 medium. Trays are placed in an environmental chamber and grown at 12hr daytime/12hr nighttime cycles. The daytime temperature is approximately 29°C and the nighttime temperature approximately 24°C. Soil is checked and watered daily to maintain even

15   moisture conditions. Tissue is collected 2 days after the start of imbibition. The 2 days after imbibition samples are separated into 3 collections after removal of any adhering seed coat. At the 2 day stage, the hypocotyl axis is emerging from the soil. A few seedlings have cracked the soil surface and exhibited slight greening of the exposed cotyledons. The seedlings are washed in water to remove soil, hypocotyl axis harvested and immediately frozen in liquid nitrogen. The

20   harvested tissue is then stored at −80°C until RNA preparation. The RNA is purified from the stored tissue and the cDNA library is constructed as described in Example 2.

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The SOYMON004 cDNA library is generated from soybean cultivar Asgrow 3244

(Asgrow Seed Company, Des Moines, Iowa U.S.A.) seedling cotyledon tissue harvested 2 day

post-imbibition. Seeds are planted at a depth of approximately 2cm into 2-3 inch peat pots

containing Metromix 350 medium. Trays are placed in an environmental chamber and grown at

5   12hr daytime/12hr nighttime cycles. The daytime temperature is approximately 29°C and the

nighttime temperature approximately 24°C. Soil is checked and watered daily to maintain even

moisture conditions. Tissue is collected 2 days after the start of imbibition. The 2 days after

imbibition samples are separated into 3 collections after removal of any adhering seed coat. At

the 2 day stage, the hypocotyl axis is emerging from the soil. A few seedlings have cracked the

10   soil surface and exhibited slight greening of the exposed cotyledons. The seedlings are washed

in water to remove soil, hypocotyl axis harvested and immediately frozen in liquid nitrogen. The

harvested tissue is then stored at –80°C until RNA preparation. The RNA is purified from the

stored tissue and the cDNA library is constructed as described in Example 2.

    The SOYMON005 cDNA library is generated from soybean cultivar Asgrow 3244

15   (Asgrow Seed Company, Des Moines, Iowa U.S.A.) seedling hypocotyl axis tissue harvested 6

hour post-imbibition. Seeds are planted at a depth of approximately 2cm into 2-3 inch peat pots

containing Metromix 350 medium. Trays are placed in an environmental chamber and grown at

12hr daytime/12hr nighttime cycles. The daytime temperature is approximately 29°C and the

nighttime temperature approximately 24°C. Soil is checked and watered daily to maintain even

20   moisture conditions. Tissue is collected 6 hours after the start of imbibition. The 6 hours after

imbibition samples are separated into 3 collections after removal of any adhering seed coat. The

6 hours after imbibition sample is collected over the course of approximately 2 hours starting at 6

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hours post imbibition. At the 6 hours after imbibition stage, not all cotyledons have become

fully hydrated and germination, or radicle protrusion, has not occurred. The seedlings are

washed in water to remove soil, hypocotyl axis harvested and immediately frozen in liquid

nitrogen. The harvested tissue is then stored at −80°C until RNA preparation. The RNA is

5   purified from the stored tissue and the cDNA library is constructed as described in Example 2.

The SOYMON006 cDNA library is generated from soybean cultivar Asgrow 3244

(Asgrow Seed Company, Des Moines, Iowa U.S.A.) seedling cotyledons tissue harvested 6 hour

post-imbibition. Seeds are planted at a depth of approximately 2cm into 2-3 inch peat pots

containing Metromix 350 medium. Trays are placed in an environmental chamber and grown at

10   12hr daytime/12hr nighttime cycles. The daytime temperature is approximately 29°C and the

nighttime temperature approximately 24°C. Soil is checked and watered daily to maintain even

moisture conditions. Tissue is collected 6 hours after imbibition. The 6 hours after imbibition

samples are separated into 3 collections after removal of any adhering seed coat. The 6 hours

after imbibition sample is collected over the course of approximately 2 hours starting at 6 hours

15   post-imbibition. At the 6 hours after imbibition, not all cotyledons have become fully hydrated

and germination or radicle protrusion, have not occurred. The seedlings are washed in water to

remove soil, cotyledon harvested and immediately frozen in liquid nitrogen. The harvested

tissue is then stored at −80°C until RNA preparation. The RNA is purified from the stored tissue

and the cDNA library is constructed as described in Example 2.

20   The SOYMON007 cDNA library is generated from soybean cultivar Asgrow 3244

(Asgrow Seed Company, Des Moines, Iowa U.S.A.) seed tissue harvested 25 and 35 days post-

flowering. Seed pods from field grown plants are harvested 25 and 35 days after flowering and

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the seeds extracted from the pods. Approximately 4.4g and 19.3g of seeds are harvested from the respective seed pods and immediately frozen in dry ice. The harvested tissue is then stored at −80°C until RNA preparation. The RNA is purified from the stored tissue and the cDNA library is constructed as described in Example 2.

5   The SOYMON008 cDNA library is generated from soybean cultivar Asgrow 3244 (Asgrow Seed Company, Des Moines, Iowa U.S.A.) leaf tissue harvested from 25 and 35 days post-flowering plants. Total leaf tissue is harvested from field grown plants. Approximately 19g and 29g of leaves are harvested from the fourth node of the plant 25 and 35 days post-flowering and immediately frozen in dry ice. The harvested tissue is then stored at −80°C until RNA

10   preparation. The RNA is purified from the stored tissue and the cDNA library is constructed as described in Example 2.

      The SOYMON009 cDNA library is generated from soybean cutlivar C1944 (USDA Soybean Germplasm Collection, Urbana, Illinois U.S.A.) pod and seed tissue harvested 15 days post-flowering. Pods from field grown plants are harvested 15 days post-flowering.

15   Approximately 3g of pod tissue is harvested and immediately frozen in dry-ice. The harvested tissue is then stored at −80°C until RNA preparation. The RNA is purified from the stored tissue and the cDNA library is constructed as described in Example 2.

      The SOYMON010 cDNA library is generated from soybean cultivar C1944 (USDA Soybean Germplasm Collection, Urbana, Illinois U.S.A.) seed tissue harvested 40 days post-

20   flowering. Pods from field grown plants are harvested 40 days post-flowering. Pods and seeds are separated, approximately 19g of seed tissue is harvested and immediately frozen in dry-ice.

The harvested tissue is then stored at −80°C until RNA preparation. The RNA is purified from the stored tissue and the cDNA library is constructed as described in Example 2.

The SOYMON011 cDNA library is generated from soybean cultivars Cristalina (USDA Soybean Germplasm Collection, Urbana, Illinois U.S.A.) and FT108 (Monsoy, Brazil) (tropical germ plasma) leaf tissue. Leaves are harvested from plants grown in an environmental chamber under 12hr daytime/12hr nighttime cycles. The daytime temperature is approximately 29°C and the nighttime temperature approximately 24°C. Soil is checked and watered daily to maintain even moisture conditions. Approximately 30g of leaves are harvested from the 4th node of each of the Cristalina and FT108 cultivars and immediately frozen in dry ice. The harvested tissue is then stored at −80°C until RNA preparation. The RNA is purified from the stored tissue and the cDNA library is constructed as described in Example 2.

The SOYMON012 cDNA library is generated from soybean cultivar Asgrow 3244 (Asgrow Seed Company, Des Moines, Iowa U.S.A.) leaf tissue. Leaves from field grown plants are harvested from the fourth node 15 days post-flowering. Approximately 12g of leaves are harvested and immediately frozen in dry ice. The harvested tissue is then stored at −80°C until RNA preparation. The RNA is purified from the stored tissue and the cDNA library is constructed as described in Example 2.

The SOYMON013 cDNA library is generated from soybean cultivar Asgrow 3244 (Asgrow Seed Company, Des Moines, Iowa U.S.A.) root and nodule tissue. Approximately, 28g of root tissue from field grown plants is harvested 15 days post-flowering. The root system is cut from the soybean plant, washed with water to free it from the soil and immediately frozen in dry-

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ice. The harvested tissue is then stored at −80°C until RNA preparation. The RNA is purified

from the stored tissue and the cDNA library is constructed as described in Example 2.

The SOYMON014 cDNA library is generated from soybean cultivar Asgrow 3244

(Asgrow Seed Company, Des Moines, Iowa U.S.A.) seed tissue harvested 25 and 35 days after

5   flowering. Seed pods from field grown plants are harvested 15 days after flowering and the

seeds extracted from the pods. Approximately 5g of seeds are harvested from the respective seed

pods and immediately frozen in dry ice. The harvested tissue is then stored at −80°C until RNA

preparation. The RNA is purified from the stored tissue and the cDNA library is constructed as

described in Example 2.

10   The SOYMON015 cDNA is generated from soybean cultivar Asgrow 3244 (Asgrow

Seed Company, Des Moines, Iowa U.S.A.) seed tissue harvested 45 and 55 days post-flowering.

Seed pods from field grown plants are harvested 45 and 55 days after flowering and the seeds

extracted from the pods. Approximately 19g and 31g of seeds are harvested from the respective

seed pods and immediately frozen in dry ice. The harvested tissue is then stored at −80°C until

15   RNA preparation. The RNA is purified from the stored tissue and the cDNA library is

constructed as described in Example 2.

The SOYMON016 cDNA library is generated from soybean cultivar Asgrow 3244

(Asgrow Seed Company, Des Moines, Iowa U.S.A.) root tissue. Approximately, 61g and 38g of

root tissue from field grown plants is harvested 25 and 35 days post- flowering is harvested. The

20   root system is cut from the soybean plant and washed with water to free it from the soil. The

tissue is placed in 14ml polystyrene tubes and immediately frozen in dry-ice. The harvested

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tissue is then stored at –80°C until RNA preparation. The RNA is purified from the stored tissue and the cDNA library is constructed as described in Example 2.

The SOYMON017 cDNA library is generated from soybean cultivar Asgrow 3244 (Asgrow Seed Company, Des Moines, Iowa U.S.A.) root tissue. Approximately 28g of root tissue from field grown plants is harvested 45 and 55 days post-flowering. The root system is cut from the soybean plant, washed with water to free it from the soil and immediately frozen in dry-ice. The harvested tissue is then stored at –80°C until RNA preparation. The RNA is purified from the stored tissue and the cDNA library is constructed as described in Example 2.

The SOYMON018 cDNA is generated from soybean cultivar Asgrow 3244 (Asgrow Seed Company, Des Moines, Iowa U.S.A.) leaf tissue harvested 45 and 55 days post-flowering. Leaves from field grown plants are harvested 45 and 55 days after flowering from the fourth node. Approximately 27g and 33g of seeds are harvested from the respective seed pods and immediately frozen in dry ice. The harvested tissue is then stored at –80°C until RNA preparation. The RNA is purified from the stored tissue and the cDNA library is constructed as described in Example 2.

The SOYMON019 cDNA library is generated from soybean cultivars Cristalina (USDA Soybean Germplasm Collection, Urbana, Illinois U.S.A.) and FT108 (Monsoy, Brazil) (tropical germ plasma) root tissue. Roots are harvested from plants grown in an environmental chamber under 12hr daytime/12hr nighttime cycles. The daytime temperature is approximately 29°C and the nighttime temperature approximately 24°C. Soil is checked and watered daily to maintain even moisture conditions. Approximately 50g and 56g of roots are harvested from each of the Cristalina and FT108 cultivars and immediately frozen in dry ice. The harvested tissue is then

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stored at −80°C until RNA preparation. The RNA is purified from the stored tissue and the cDNA library is constructed as described in Example 2.

The SOYMON020 cDNA is generated from soybean cultivar Asgrow 3244 (Asgrow Seed Company, Des Moines, Iowa U.S.A.) seed tissue harvested 65 and 75 days post-flowering. Seed pods from field grown plants are harvested 45 and 55 days after flowering and the seeds extracted from the pods. Approximately 14g and 31g of seeds are harvested from the respective seed pods and immediately frozen in dry ice. The harvested tissue is then stored at −80°C until RNA preparation. The RNA is purified from the stored tissue and the cDNA library is constructed as described in Example 2.

The SOYMON021 cDNA library is generated from Soybean Cyst Nematode-resistant soybean cultivar Hartwig (USDA Soybean Germplasm Collection, Urbana, Illinois U.S.A.) root tissue. Plants are grown in tissue culture at room temperature. At approximately 6 weeks post-germination, the plants are exposed to sterilized Soybean Cyst Nematode eggs. Infection is then allowed to progress for 10 days. After the 10 day infection process, the tissue is harvested. Agar from the culture medium and nematodes are removed and the root tissue is immediately frozen in dry ice. The harvested tissue is then stored at −80°C until RNA preparation. The RNA is purified from the stored tissue and the cDNA library is constructed as described in Example 2.

The SOYMON022 (Lib3030) cDNA library is generated from soybean cultivar Asgrow 3244 (Asgrow Seed Company, Des Moines, Iowa U.S.A.) partially opened flower tissue. Partially to fully opened flower tissue is harvested from plants grown in an environmental chamber under 12hr daytime/12hr nighttime cycles. The daytime temperature is approximately 29°C and the nighttime temperature approximately 24°C. Soil is checked and watered daily to

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maintain even moisture conditions. A total of 3g of flower tissue is harvested and immediately

frozen in dry ice. The harvested tissue is then stored at −80°C until RNA preparation. The RNA

is purified from the stored tissue and the cDNA library is constructed as described in Example 2.

The SOYMON023 cDNA library is generated from soybean genotype BW211S Null

5   (Tohoku University, Morioka, Japan) seed tissue harvested 15 and 40 days post-flowering. Seed

pods from field grown plants are harvested 15 and 40 days post-flowering and the seeds extracted

from the pods. Approximately 0.7g and 14.2g of seeds are harvested from the respective seed

pods and immediately frozen in dry ice. The harvested tissue is then stored at −80°C until RNA

preparation. The RNA is purified from the stored tissue and the cDNA library is constructed as

10   described in Example 2.

The SOYMON024 cDNA library is generated from soybean cultivar Asgrow 3244

(Asgrow Seed Company, Des Moines, Iowa U.S.A.) internode-2 tissue harvested 18 days post-

imbibition. Seeds are planted at a depth of approximately 2cm into 2-3 inch peat pots containing

Metromix 350 medium. The plants are grown in a greenhouse for 18 days after the start of

15   imbibition at ambient temperature. Soil is checked and watered daily to maintain even moisture

conditions. Stem tissue is harvested 18 days after the start of imbibition. The samples are

divided into hypocotyl and internodes 1 through 5. The fifth internode contains some leaf bud

material. Approximately 3 g of each sample is harvested and immediately frozen in dry ice. The

harvested tissue is then stored at −80°C until RNA preparation. The RNA is purified from the

20   stored tissue and the cDNA library is constructed as described in Example 2.

The SOYMON025 cDNA library is generated from soybean cultivar Asgrow 3244

(Asgrow Seed Company, Des Moines, Iowa U.S.A.) leaf tissue harvested 65 days post-flowering.

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Leaves are harvested from the fourth node of field grown plants 65 days post-flowering. Approximately 18.4g of leaf tissue is harvested and immediately frozen in dry ice. The harvested tissue is then stored at −80°C until RNA preparation. The RNA is purified from the stored tissue and the cDNA library is constructed as described in Example 2.

5   SOYMON026 cDNA library is generated from soybean cultivar Asgrow 3244 (Asgrow Seed Company, Des Moines, Iowa U.S.A.) root tissue harvested 65 and 75 days post-flowering. Approximately 27g and 40g of root tissue from field grown plants is harvested 65 and 75 days post- flowering. The root system is cut from the soybean plant, washed with water to free it from the soil and immediately frozen in dry-ice. The harvested tissue is then stored at −80°C until

10   RNA preparation. The RNA is purified from the stored tissue and the cDNA library is constructed as described in Example 2.

The SOYMON027 cDNA library is generated from soybean cultivar Asgrow 3244 (Asgrow Seed Company, Des Moines, Iowa U.S.A.) pod tissue, without seeds, harvested 25 days post-flowering. Seed pods from field grown plants are harvested 25 days post-flowering and the

15   seeds extracted from the pods. Approximately 17g of seed pod tissue is harvested and immediately frozen in dry ice. The harvested tissue is then stored at -80°C until RNA preparation. The RNA is purified from the stored tissue and the cDNA library is constructed as described in Example 2.

The SOYMON028 cDNA library is generated from soybean cultivar Asgrow 3244

20   (Asgrow Seed Company, Des Moines, Iowa U.S.A.) drought-stressed root tissue. The plants are grown in an environmental chamber under 12hr daytime/12hr nighttime cycles. The daytime temperature is approximately 29°C and the nighttime temperature 24°C. Soil is checked and

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watered daily to maintain even moisture conditions. At the R3 stage of development, water is

withheld from half of the plant collection (drought stressed population). After 3 days, half of the

plants from the drought stressed condition and half of the plants from the control population are

harvested. After another 3 days (6 days post drought induction) the remaining plants are

5 harvested. A total of 27g and 40g of root tissue is harvested and immediately frozen in dry ice.

The harvested tissue is then stored at –80°C until RNA preparation. The RNA is purified from

the stored tissue and the cDNA library is constructed as described in Example 2.

The SOYMON029 cDNA library is generated from Soybean Cyst Nematode-resistant

soybean cultivar PI07354 (USDA Soybean Germplasm Collection, Urbana, Illinois U.S.A.) root

10 tissue. Late fall to early winter greenhouse grown plants are exposed to Soybean Cyst Nematode

eggs. At 10 days post-infection, the plants are uprooted, rinsed briefly and the roots frozen in

liquid nitrogen. Approximately 20 grams of root tissue is harvested from the infected plants.

The harvested tissue is then stored at –80°C until RNA preparation. The RNA is purified from

the stored tissue and the cDNA library is constructed as described in Example 2.

15 The SOYMON030 cDNA library is generated from soybean cultivar Asgrow 3244

(Asgrow Seed Company, Des Moines, Iowa U.S.A.) flower bud tissue. Seeds are planted at a

depth of approximately 2cm into 2-3 inch peat pots containing Metromix 350 medium and the

plants are grown in an environmental chamber under 12hr daytime/12hr nighttime cycles. The

daytime temperature is approximately 29°C and the nighttime temperature approximately 24°C.

20 Soil is checked and watered daily to maintain even moisture conditions. Flower buds are

removed from the plant at the pedicel. A total of 100mg of flower buds are harvested and

immediately frozen in liquid nitrogen. The harvested tissue is then stored at –80°C until RNA

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preparation.Total RNA is prepared from 50 mg of tissue and used directly to generate a library using the Clonetech SMART™ PCR cDNA (Palo Alto, California (U.S.A.) library construction kit. The EcoRI/XhoI adaptors are used in this library construction. The cDNA is ligated into the pINCY vector.

5   The SOYMON031 cDNA library is generated from soybean cultivar Asgrow 3244 (Asgrow Seed Company, Des Moines, Iowa U.S.A.) carpel and stamen tissue. Seeds are planted at a depth of approximately 2cm into 2-3 inch peat pots containing Metromix 350 medium and the plants are grown in an environmental chamber under 12hr daytime/12hr nighttime cycles. The daytime temperature is approximately 29°C and the nighttime temperature approximately

10   24°C. Soil is checked and watered daily to maintain even moisture conditions. Flower buds are removed from the plant at the pedicel. Flowers are dissected to separate petals, sepals and reproductive structures (carpels and stamens). A total of 300mg of carpel and stamen tissue are harvested and immediately frozen in liquid nitrogen. The harvested tissue is then stored at –80°C until RNA preparation. Total RNA is prepared from 150 mg of tissue and used directly to

15   generate a library using the Clonetech SMART™ PCR cDNA(Palo Alto, California (U.S.A.) library construction kit. The EcoRI/XhoI adaptors are used in this library construction. The cDNA is ligated into the pINCY vector.

The SOYMON032 cDNA library is prepared from the Asgrow cultivar A4922 (Asgrow Seed Company, Des Moines, Iowa U.S.A.) rehydrated dry soybean seed meristem tissue.

20   Surface sterilized seeds are germinated in liquid media for 24 hours. The seed axis is then excised from the barely germinating seed, placed on tissue culture media and incubated overnight at 20°C in the dark. The supportive tissue is removed from the explant prior to harvest.

Approximately 570mg of tissue is harvested and frozen in liquid nitrogen. The harvested tissue is then stored at −80°C until RNA preparation. The RNA is purified from the stored tissue and the cDNA library is constructed as described in Example 2.

The SOYMON033 cDNA library is generated from soybean cultivar Asgrow 3244

5 (Asgrow Seed Company, Des Moines, Iowa U.S.A.) heat-shocked seedling tissue without cotyledons. Seeds are imbibed and germinated in vermiculite for 2 days under constant illumination. After 48 hours, the seedlings are transferred to an incubator set at 40°C under constant illumination. After 30, 60 and 180 minutes seedlings are harvested and dissected. A portion of the seedling consisting of the root, hypocotyl and apical hook is frozen in liquid

10 nitrogen and stored at −80°C. The seedlings after 2 days of imbibition are beginning to emerge from the vermiculite surface. The apical hooks are dark green in appearance. Total RNA and poly A⁺ RNA is prepared from equal amounts of pooled tissue. The RNA is purified from the stored tissue and the cDNA library is constructed as described in Example 2.

The SOYMON034 cDNA library is generated from soybean cultivar Asgrow 3244

15 (Asgrow Seed Company, Des Moines, Iowa U.S.A.) cold-shocked seedling tissue without cotyledons. Seeds are imbibed and germinated in vermiculite for 2 days under constant illumination. After 48 hours, the seedlings are transferred to a cold room set at 5°C under constant illumination. After 30, 60 and 180 minutes seedlings are harvested and dissected. The seedlings after 2 days of imbibition are beginning to emerge from the vermiculite surface. The

20 apical hooks are dark green in appearance. A portion of the seedling consisting of the root, hypocotyl and apical hook is frozen in liquid nitrogen and stored at −80°C. The RNA is purified from the stored tissue and the cDNA library is constructed as described in Example 2.

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The SOYMON035 cDNA library is generated from soybean cultivar Asgrow 3244

(Asgrow Seed Company, Des Moines, Iowa U.S.A.) seed coat tissue. Seeds are planted at a

depth of approximately 2cm into 2-3 inch peat pots containing Metromix 350 medium and the

plants are grown in an environmental chamber under 12hr daytime/12hr nighttime cycles. The

5   daytime temperature is approximately 29°C and the nighttime temperature 24°C. Soil is checked

and watered daily to maintain even moisture conditions. Seeds are harvested from mid to nearly

full maturation (seed coats are not yellowing). The entire embryo proper is removed from the

seed coat sample and the seed coat tissue are harvested and immediately frozen in liquid

nitrogen. The harvested tissue is then stored at –80°C until RNA preparation. The RNA is

10   purified from the stored tissue and the cDNA library is constructed as described in Example 2.

The SOYMON036 cDNA library is generated from soybean cultivars PI171451,

PI227687 and PI229358 (USDA Soybean Germplasm Collection, Urbana, Illinois U.S.A.) insect

challenged leaves. Plants from each of the three cultivars are grown in screenhouse conditions.

The screenhouse is divided in half and one half of the screenhouse is infested with soybean

15   looper and the other half infested with velvetbean caterpillar. A single leaf is taken from each of

the representative plants at 3 different time points, 11 days after infestation, 2 weeks after

infestation and 5 weeks after infestation and immediately frozen in liquid nitrogen. The

harvested tissue is then stored at –80°C until RNA preparation. Total RNA and poly A+ RNA is

isolated from pooled tissue consisting of equal quantities of all 18 samples (3 genotypes X 3

20   sample times X 2 insect genotypes). The RNA is purified from the stored tissue and the cDNA

library is constructed as described in Example 2.

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The SOYMON037 cDNA library is generated from soybean cultivar A3244 (Asgrow

Seed Company, Des Moines, Iowa U.S.A.) etiolated axis and radical tissue. Seeds are planted in

moist vermiculite, wrapped and kept at room temperature in complete darkness until harvest.

Etiolated axis and hypocotyl tissue is harvested at 2, 3 and 4 days post-planting. A total of 1

gram of each tissue type is harvested at 2, 3 and 4 days after planting and immediately frozen in

liquid nitrogen. The harvested tissue is then stored at −80°C until RNA preparation. The RNA is

purified from the stored tissue and the cDNA library is constructed as described in Example 2.

The SOYMON038 cDNA library is generated from soybean variety Asgrow A3237

(Asgrow Seed Company, Des Moines, Iowa U.S.A.) rehydrated dry seeds. Explants are prepared

for transformation after germination of surface-sterilized seeds on solid tissue media. After

6days, at 28°C and 18 hours of light per day, the germinated seeds are cold shocked at 4°C for 24

hours. Meristemic tissue and part of the hypocotyl is remove and cotyledon excised. The

prepared explant is then wounded for *Agrobacterium* infection. The 2 grams of harvested tissue

is frozen in liquid nitrogen and stored at −80°C until RNA preparation. The RNA is purified

from the stored tissue and the cDNA library is constructed as described in Example 2.

The Soy51 (LIB3027) normalized cDNA library is prepared from pooled seeds from

SOYMON007, SOYMON015 and SOYMON020. Equal amounts of SOYMON007,

SOYMON015, and SOYMON020 in the form of single stranded DNA, are mixed and used as

the starting material for normalization. The normalized cDNA library is constructed as described

in Example 2.

The Soy52 (LIB3028) normalized cDNA library is generated from flowers collected from

soybean cultivar Asgrow 3244 (Asgrow Seed Company, Des Moines, Iowa U.S.A.) plants. The

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tissue descriptions for this library are identical to that for Soy35 (SOYMON022). The RNA is purified from the stored tissue and the normalized cDNA library is constructed as described in Example 2.

The Soy53 (LIB3039) cDNA library is generated from soybean cultivar Asgrow 3244 (Asgrow Seed Company, Des Moines, Iowa U.S.A.) seedling shoot apical meristem tissue. Seeds are planted at a depth of approximately 2cm into 2-3 inch peat pots containing Metromix 350 medium and the plants are grown in an environmental chamber under 12hr daytime/12hr nighttime cycles. The daytime temperature is approximately 29°C and the nighttime temperature 24°C. Soil is checked and watered daily to maintain even moisture conditions. Apical tissue is harvested from seedling shoot meristem tissue, 7-8 days after the start of imbibition. The apex of each seedling is dissected to include the fifth node to the apical meristem. The fifth node corresponds to the third trifoliate leaf in the very early stages of development. Stipules completely envelop the leaf primordia at this time. A total of 200mg of apical tissue is harvested and immediately frozen in liquid nitrogen. The harvested tissue is then stored at −80°C until RNA preparation. The RNA is purified from the stored tissue and the cDNA library is constructed as described in Example 2.

The Soy54 (LIB3040) cDNA library is generated from soybean cultivar Asgrow 3244 (Asgrow Seed Company, Des Moines, Iowa U.S.A.) heart to torpedo stage embryo tissue. Seeds are planted at a depth of approximately 2cm into 2-3 inch peat pots containing Metromix 350 medium and the plants are grown in an environmental chamber under 12hr daytime/12hr nighttime cycles. The daytime temperature is approximately 29°C and the nighttime temperature 24°C. Soil is checked and watered daily to maintain even moisture conditions. Seeds are

collected and embryos removed from surrounding endosperm and maternal tissues. Embryos from globular to young torpedo stages (by corresponding analogy to *Arabidopsis*) are collected with a bias towards the middle of this spectrum. Embryos which are beginning to show asymmetric development of cotyledons are considered the upper developmental boundary for the

5   collection and are excluded. A total of 12 mg embryo tissue is frozen in liquid nitrogen. The harvested tissue is stored at –80°C until RNA preparation. Total RNA is prepared from 100 mg of tissue and used directly to generate a library using the Clonetech SMART™ PCR cDNA(Palo Alto, California (U.S.A.)) library construction kit. The SalI adaptors are used in this library construction. The cDNA is ligated into the pSPORT vector.

10   Soy55 (LIB3049) cDNA library is generated from soybean cultivar Asgrow 3244 (Asgrow Seed Company, Des Moines, Iowa U.S.A.) young seed tissue. Seeds are planted at a depth of approximately 2cm into 2-3 inch peat pots containing Metromix 350 medium and the plants are grown in an environmental chamber under 12hr daytime/12hr nighttime cycles. The daytime temperature is approximately 29°C and the nighttime temperature 24°C. Soil is checked

15   and watered daily to maintain even moisture conditions. Seeds are collected from very young pods (5 to 15 days after flowering). A total of 100mg of seeds are harvested and frozen in liquid nitrogen. The harvested tissue is stored at –80°C until RNA preparation. Total RNA is prepared from 100 mg of tissue and used directly to generate a library using the Clonetech SMART™ PCR cDNA(Palo Alto, California (U.S.A.)) library construction kit. The SalI adaptors are used

20   in this library construction. The cDNA is ligated into the pSPORT vector.

Soy56 (LIB3029) cDNA library is prepared from pooled seeds from Soy19 (SOYMON007), Soy27 (SOYMON015) and Soy33 (SOYMON020). Equal amounts of Soy19,

Soy27 and Soy33, in the form of single stranded DNA, are mixed in equimolar quantities. This mixture is used as a non-normalized control for comparison to Soy51. The cDNA library is constructed as described in Example 2.

TheSoy58 (LIB3050) cDNA library is generated from soybean cultivar Asgrow 3244
5   (Asgrow Seed Company, Des Moines, Iowa U.S.A.) drought stressed root tissue subtracted from control root tissue. Seeds are planted at a depth of approximately 2cm into 2-3 inch peat pots containing Metromix 350 medium and the plants are grown in an environmental chamber under 12hr daytime/12hr nighttime cycles. The daytime temperature is approximately 29°C and the nighttime temperature 24°C. Soil is checked and watered daily to maintain even moisture
10   conditions. At the R3 stage of the plant drought is induced by withholding water. After 3 and 6 days root tissue from both drought stressed and control (watered regularly) plants are collected and frozen in dry-ice. The harvested tissue is stored at –80°C until RNA preparation. The RNA is prepared from the stored tissue and the subtracted cDNA library is constructed as described in Example 2.

15   The Soy59 (LIB3051) cDNA library is generated from soybean cultivar Asgrow 3244 (Asgrow Seed Company, Des Moines, Iowa U.S.A.) endosperm tissue. Seeds are germinated on paper towels under laboratory ambient light conditions. At 8, 10 and 14 hours after imbibition, the seed coats are harvested. The endosperm consists of a very thin layer of tissue affixed to the inside of the seed coat. The seed coat and endosperm are frozen immediately after harvest in
20   liquid nitrogen. The harvested tissue is stored at –80°C until RNA preparation. The RNA is prepared from the stored tissue and the cDNA library is constructed using the pSPORT cDNA

synthesis kit from Life Technologies (Life Technologies, Gaithersburg, Maryland U.S.A.). The resulting cDNA is ligated into the pSPORT.

The Soy60 (LIB3072) cDNA library is generated by subtracting the target cDNA, which is prepared from soybean cultivar Asgrow 3244 (Asgrow Seed Company, Des Moines, Iowa U.S.A.) seeds plus pods from drought stressed plants, from the driver cDNA, which is prepared from soybean cultivar Asgrow 3244 seeds plus pods from non drought-stressed (control) plants. Seeds are planted at a depth of approximately 2cm into 2-3 inch peat pots containing Metromix 350 medium and the plants are grown in an environmental chamber under 12hr daytime/12hr nighttime cycles. The daytime temperature is approximately 26°C and the nighttime temperature 21°C and 70% relative humidity. Soil is checked and watered daily to maintain even moisture conditions. At the R3 stage of the plant drought is induced by withholding water. After 3 and 6 days seeds and pods from both drought stressed and control (watered regularly) plants are collected from the fifth and sixth node and frozen in dry-ice. The harvested tissue is stored at –80°C until RNA preparation. The RNA is prepared from the stored tissue and the subtracted cDNA library is constructed as described in Example 2.

The Soy61 (LIB3073) cDNA library is generated by subtracting the target cDNA, which is prepared from soybean cultivar Asgrow 3244 (Asgrow Seed Company, Des Moines, Iowa U.S.A.) jasmonic acid treated seedling, from the driver cDNA, which is prepared from control buffer treated seedlings without cotyledon. Seeds are planted at a depth of approximately 2cm into 2-3 inch peat pots containing Metromix 350 medium and the plants are grown in a greenhouse. The daytime temperature is approximately 29.4°C and the nighttime temperature 20°C. Soil is checked and watered daily to maintain even moisture conditions. At 9 days post

planting, the plantlets are sprayed with either control buffer of 0.1% Tween-20 or jasmonic acid

(Sigma J-2500, Sigma, St. Louis, Missouri U.S.A.) at 1 mg/ml in 0.1% Tween-20. Plants are

sprayed until runoff and the soil and the stem is socked with the spraying solution. At 18 hours

post application of jasmonic acid, the soybean plantlets appear growth retarded. After 18 hours,

5   24 hours and 48 hours post treatment, the cotyledons are removed and the remaining leaf and

stem tissue above the soil is harvested and frozen in liquid nitrogen. The harvested tissue is

stored at −80°C until RNA preparation. To make RNA, the three sample timepoints were

combined and ground. The RNA is prepared from the stored tissue and the subtracted cDNA

library is constructed as described in Example 2. For this library's construction, the eighth

10   fraction of the cDNA size fractionation step was used for ligation.

The Soy62 (LIB3074) cDNA library is generated by subtracting the target cDNA, which

is prepared from soybean cultivar Asgrow 3244 (Asgrow Seed Company, Des Moines, Iowa

U.S.A.) jasmonic acid treated seedlings without cotyledon, from the driver cDNA, which is

prepared from soybean cultivar Asgrow 3244 control buffer treated seedlings without cotyledon..

15   Seeds are planted at a depth of approximately 2cm into 2-3 inch peat pots containing Metromix

350 medium and the plants are grown in a greenhouse. The daytime temperature is

approximately 29.4°C and the nighttime temperature 20°C. Soil is checked and watered daily to

maintain even moisture conditions. At 9 days post planting, the plantlets are sprayed with either

control buffer of 0.1% Tween-20 or jasmonic acid (Sigma J-2500, Sigma, St. Louis, Missouri

20   U.S.A.) at 1 mg/ml in 0.1% Tween-20. Plants are sprayed until runoff and the soil and the stem

is socked with the spraying solution. At 18 hours post application of jasmonic acid, the soybean

plantlets appear growth retarded. After 18 hours, 24 hours and 48 hours post treatment, the

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cotyledons are removed and the remaining leaf and stem tissue above the soil is harvested and

frozen in liquid nitrogen. The harvested tissue is stored at –80°C until RNA preparation. To

make RNA, the three sample timepoints were combined and ground. The RNA is prepared from

the stored tissue and the subtracted cDNA library is constructed as described in Example 2. For

5   this library's construction, the ninth fraction of the cDNA size fractionation step was used for

ligation.

The Soy65 (LIB3107) cDNA library is generated from soybean cultivar Asgrow 3244

(Asgrow Seed Company, Des Moines, Iowa U.S.A.) abscission zone tissue from drought-stressed

plants. Seeds are planted at a depth of approximately 2cm into 2-3 inch peat pots containing

10   Metromix 350 medium and the plants are grown in an environmental chamber under 12hr

daytime/12hr nighttime cycles. The daytime temperature is approximately 29°C and the

nighttime temperature 24°C. Soil is checked and watered daily to maintain even moisture

conditions. Plants are irrigated with 15-16-17 Peter's Mix. At the R3 stage of development,

drought is imposed by withholding water. At 3, 4, 5 and 6 days, tissue is harvested and wilting is

15   not obvious until the fourth day. Abscission layers from reproductive organs are harvested by

cutting less than one millimeter proximal and distal to the layer and immediately frozen in liquid

nitrogen. The harvested tissue is stored at –80°C until RNA preparation. The following tissues

are combined for the single library: four day stress, all nodes; 5 day stress, all nodes The RNA is

prepared from the stored tissue and the cDNA library is constructed as described in Example 2.

20   The Soy66 (LIB3109) cDNA library is generated from soybean cultivar Asgrow 3244

(Asgrow Seed Company, Des Moines, Iowa U.S.A.) abscission zone tissue from control (watered

regularly) plants. Seeds are planted at a depth of approximately 2cm into 2-3 inch peat pots

containing Metromix 350 medium and the plants are grown in an environmental chamber under 12hr daytime/12hr nighttime cycles. The daytime temperature is approximately 29°C and the nighttime temperature approximately 24°C. Soil is checked and watered daily to maintain even moisture conditions. Plants are irrigated with 15-16-17 Peter's Mix. At 3, 4, 5 and 6 days

5   (relative to drought stress induction in plants for soy65), abscission layer tissue is harvested. Abscission layers from reproductive organs are harvested by cutting less than one millimeter proximal and distal to the layer and immediately frozen in liquid nitrogen. The harvested tissue is stored at –80°C until RNA preparation. The following samples are combined for this cDNA library: 4 day control, all nodes; 5 day control; all nodes. The RNA is prepared from the stored

10   tissue and the cDNA library is constructed as described in Example 2.

Soy67 (LIB3065) normalized cDNA library is prepared from pooled seeds from SOYMON007, SOYMON015 and SOYMON020 prepared tissue. Equal amounts of Soy19 (SOYMON007), Soy27 (SOYMON015) and Soy33 (SOYMON020), in the form of single stranded DNA, are mixed and used as the starting material for normalization. The normalized

15   cDNA library is constructed as described in Example 2.

Soy68 (LIB3052) normalized cDNA library is prepared from pooled seeds from SOYMON007, SOYMON015 and SOYMON020. Equal amounts of Soy19 (SOYMON007), Soy27 (SOYMON015) and Soy33 (SOYMON020), in the form of single stranded DNA, are mixed and used as the starting material for normalization. The normalized cDNA library is

20   constructed as described in Example 2.

Soy69 (LIB3053) normalized cDNA library is generated from soybean cultivars Cristalina (USDA Soybean Germplasm Collection, Urbana, Illinois U.S.A.) and FT108

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(Monsoy, Brazil) (tropical germ plasma) normalized leaf tissue. Leaves are harvested from plants grown in an environmental chamber under 12hr daytime/12hr nighttime cycles. The daytime temperature is approximately 29°C and the nighttime temperature approximately 24°C. Soil is checked and watered daily to maintain even moisture conditions. Approximately 30g of leaves are harvested from the 4th node of each of the Cristalina and FT108 cultivars and immediately frozen in dry ice. The harvested tissue is then stored at −80°C until RNA preparation. The RNA is prepared from the stored tissue and the normalized cDNA library is constructed as described in Example 2.

LIB3054 is a normalized cDNA library generated from roots from two exotic soybean cultivars Cristilliana and FT108 (Monsoy, Brazil, tropical germ plasma). The roots are harvested from plants grown an environmental chamber set to a 12h day/12h night cycle, 29°C daytime temperature, 24°C night temperature and 70% relative humidity. Daytime light levels are measured at 450μEinsteins/m^2. Soil is checked and watered daily to maintain even moisture conditions. Approximately 50g and 56g of roots are collected from each of the Cristilliana and FT108 cultivars. The plants are uprooted and the roots quickly rinsed in a pail of water. The root tissue is then cut from the plants, placed immediately in 14ml polystyrene tubes and immersed in dry-ice. The tissue is then transferred to a -80°C freezer for storage. Total RNA is prepared from the combination of equal amounts of root tissue from each cultivar. The RNA is prepared from the stored tissue and the normalized cDNA library is constructed as described in Example 2.

Soy70 (LIB3055) cDNA library is generated from soybean cultivars Cristalina (USDA Soybean Germplasm Collection, Urbana, Illinois U.S.A.) and FT108 (Monsoy, Brazil) (tropical

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germ plasma) leaf tissue. Leaves are harvested from plants grown in an environmental chamber under 12hr daytime/12hr nighttime cycles. The daytime temperature is approximately 29°C and the nighttime temperature approximately 24°C. Soil is checked and watered daily to maintain even moisture conditions. Approximately 30g of leaves are harvested from the 4th node of each of the Cristalina and FT108 cultivars and immediately frozen in dry ice. The harvested tissue is then stored at −80°C until RNA preparation. The RNA is prepared from the stored tissue and the cDNA library is constructed as described in Example 2.

Soy71 (LIB3056) cDNA library is generated from soybean cultivars Cristalina and FT108 (tropical germ plasma) root tissue. Roots are harvested from plants grown in an environmental chamber under 12hr daytime/12hr nighttime cycles. The daytime temperature is approximately 29°C and the nighttime temperature approximately 24°C. Soil is checked and watered daily to maintain even moisture conditions. Approximately 50g and 56g of roots are harvested from each of the Cristalina and FT108 cultivars and immediately frozen in dry ice. The harvested tissue is then stored at −80°C until RNA preparation. The RNA is prepared from the stored tissue and the cDNA library is constructed as described in Example 2.

LIB3087 is a cDNA library that is generated from soybean cultivar Asgrow 3244 (Asgrow Seed Company, Des Moines, Iowa U.S.A). Seeds are imbibed in water for 4 hours at 30°C, and then the seed coat is removed. For the 4 hr timepoint, axis tissue is immediately harvested, and flash-frozen in liquid nitrogen. For 8 and 12 hr timepoints, decoated seeds are transferred to cotton saturated with water and incubated at 30°C for the remainder of the incubation period. Axis tissue is then excised and frozen in liquid nitrogen. Equal numbers of axes from each timepoint is pooled for RNA isolation. The collected tissue is stored at -80°C.

Axis tissue consists of unexpanded root, hypocotyl, epicotyl and apex. The RNA is purified

from the stored tissue and the cDNA library is constructed as described in Example 2.

LIB3092 (Soy75) cDNA library is generated from soybean cultivar Asgrow 3244

(Asgrow Seed Company, Des Moines, Iowa U.S.A.) drought stressed leaf that is subtracted from

5   a control. Seeds are planted in moist Metromix 350 medium at a depth of approximately 2cm.

Trays are placed in an environmental chamber set to a 12h day/12h night cycle, 26°C daytime

temperature, 21°C night temperature and 70% relative humidity. Daytime light levels are

measured at 300mEinsteins/m^2. Soil is checked and watered daily to maintain even moisture

conditions. At the R3 stage of the plant, drought is induced by withholding water. After 3 and 6

10   days tissue is harvested. Leaves from both drought stressed and control (watered regularly)

plants are collected from the fifth and sixth node and frozen in dry-ice. The tissue is then

transferred to a -80°C freezer for storage. For subtraction, a standard cDNA library is

constructed in the pSPORT vector. Driver first strand cDNA is covalently linked to Dynabeads

following a protocol similar to that described in the Dynal literature. The target library is then

15   heat denatured and hybridized to the driver cDNA in 400ml 4X SSPE for five rounds of

hybridization at 68°C and 20 hours. After each hybridization, the hybridization solution is

removed from the system and the hybridized target cDNA removed from the driver by heat

denaturation in water. The refreshed driver is then reintroduced to the hybridization for the next

round of hybridization. The remaining cDNA in the hybridization solution is then used to

20   transform *E. coli* for sequencing.

Soy74 (LIB3093) cDNA library is generated from soybean cultivar Asgrow 3244

(Asgrow Seed Company, Des Moines, Iowa U.S.A.) leaves collected from control (watered

regularly) plants. Seeds are planted at a depth of approximately 2cm into 2-3 inch peat pots

containing Metromix 350 medium and the plants are grown in an environmental chamber under

12hr daytime/12hr nighttime cycles. The daytime temperature is approximately 26°C and the

nighttime temperature 21°C and 70% relative humidity. Soil is checked and watered daily to

maintain even moisture conditions. At the R3 stage of the plant drought is induced by

5   withholding water. After 3 and 6 days seeds and pods from both drought stressed and control

(watered regularly) plants are collected from the fifth and sixth node and frozen in dry-ice. The

harvested tissue from control plants is stored at –80°C until RNA preparation. The RNA is

prepared from the stored tissue and the cDNA library is constructed as described in Example 2.

LIB3094 is a normalized cDNA library that is generated from soybean cultivar Asgrow

10   3244 (Asgrow Seed Company, Des Moines, Iowa U.S.A). Seeds are imbibed in water for 4

hours at 30ºC, and then the seed coat is removed. For the 4 hr timepoint, axis tissue is

immediately harvested, and flash-frozen in liquid nitrogen. For 8 and 12 hr timepoints, decoated

seeds are transferred to cotton saturated with water and incubated at 30ºC for the remainder of

the incubation period. Axis tissue is then excised and frozen in liquid nitrogen. Equal numbers

15   of axes from each timepoint is pooled for RNA isolation. The collected tissue is stored at -80ºC.

Axis tissue consists of unexpanded root, hypocotyl, epicotyl and apex. The RNA is purified

from the stored tissue and the cDNA library is constructed as described in Example 2.

The Soy76 (Lib3106) cDNA library is generated from soybean cultivar Asgrow 3244

(Asgrow Seed Company, Des Moines, Iowa U.S.A.) jasmonic acid and arachidonic treated

20   seedlings. Seeds are planted at a depth of approximately 2cm into 2-3 inch peat pots containing

Metromix 350 medium and the plants are grown in a greenhouse. The daytime temperature is

approximately 29.4°C and the nighttime temperature 20°C. Soil is checked and watered daily to

maintain even moisture conditions. At 9 days post planting, the plantlets are sprayed with either

control buffer of 0.1% Tween-20 or jasmonic acid (Sigma J-2500, Sigma, St. Louis, Missouri

U.S.A.) at 1 mg/ml in 0.1% Tween-20. Plants are sprayed until runoff and the soil and the stem

is socked with the spraying solution. At 18 hours post application of jasmonic acid, the soybean

5   plantlets appear growth retarded. Arachidonic treated seedlings are sprayed with 1m/ml

arachidonic acid in 0.1% Tween-20. After 18hours, 24hours and 48 hours post treatment, the

cotyledons are removed and the remaining leaf and stem tissue above the soil is harvested and

frozen in liquid nitrogen. The harvested tissue is stored at −80°C until RNA preparation. To

make RNA, the three sample timepoints from the jasmonic acid treated seedlings are combined

10   and ground. RNA from the arachidonic acid treated seedlings is isolated separately. Poly A$^+$

RNA is extracted from each total RNA sample separately and combined to make a cDNA library

using approximately equal amounts of mRNA from each treatment. The cDNA library is

constructed as described in Example 2. For the construction of this cDNA library, fraction 10 of

the size fractionated cDNA is ligated into the pSPORT vector (Invitrogen, Carlsbad California

15   U.S.A.) in order to capture some of the smaller transcripts characteristic of antifungal proteins.

Soy77 (LIB3108) cDNA library is generated from soybean cultivar Asgrow 3244

(Asgrow Seed Company, Des Moines, Iowa U.S.A.) control buffer (0.1% Tween-20) treated

seedlings. Seeds are planted at a depth of approximately 2cm into 2-3 inch peat pots containing

Metromix 350 medium and the plants are grown in a greenhouse. The daytime temperature is

20   approximately 29.4°C and the nighttime temperature 20°C. Soil is checked and watered daily to

maintain even moisture conditions. At 9 days post planting, the plantlets are sprayed with either

control buffer of 0.1% Tween-20 or jasmonic acid (Sigma J-2500, Sigma, St. Louis, Missouri

U.S.A.) at 1 mg/ml in 0.1% Tween-20. Plants are sprayed until runoff and the soil and the stem is socked with the spraying solution. At 18 hours post application of jasmonic acid, the soybean plantlets appear growth retarded. After 18 hours, 24 hours and 48 hours post treatment, the cotyledons are removed and the remaining leaf and stem tissue above the soil is harvested and frozen in liquid nitrogen. The harvested tissue is stored at $-80°C$ until RNA preparation. To make RNA, the three sample timepoints from control buffer treated seedlings are combined and ground. The RNA is prepared from the stored tissue and the cDNA library is constructed as described in Example 2. For the construction of this cDNA library, fraction 10 of the size fractionated cDNA is ligated into the pSPORT vector in order to capture some of the smaller transcripts characteristic of antifungal proteins.

Soy72 (LIB3138) normalized cDNA library is generated from equal amounts of Soy5 (SOYMON001), Soy20 (SOYMON008) and Soy24 (SOYMON012), Soy28 (SOYMON018) and Soy38 (SOYMON025) in the form of double stranded DNA. These DNAs are mixed and used as the starting material for normalization. The tissue descriptions for these libraries are found above. The RNA is purified from the stored tissue and the cDNA library is constructed as described in Example 2.

Soy73 (LIB3139) normalized cDNA library is generated from equal amounts of Soy6 (SOYMON002), Soy25 (SOYMON013) and Soy29 (SOYMON016), Soy31 (SOYMON017) and Soy39 (SOYMON026) in the form of double stranded DNA. These DNAs are mixed and used as the starting material for normalization. The tissue descriptions for these libraries are found above. The RNA is purified from the stored tissue and the cDNA library is constructed as described in Example 2.

Example 2

The stored RNA is purified using Trizol reagent from Life Technologies (Gibco BRL, Life Technologies, Gaithersburg, Maryland U.S.A.), essentially as recommended by the manufacturer. Poly A+ RNA (mRNA) is purified using magnetic oligo dT beads essentially as

5   recommended by the manufacturer (Dynabeads, Dynal Corporation, Lake Success, New York U.S.A.).

Construction of plant cDNA libraries is well-known in the art and a number of cloning strategies exist. A number of cDNA library construction kits are commercially available. The Superscript™ Plasmid System for cDNA synthesis and Plasmid Cloning (Gibco BRL, Life

10   Technologies, Gaithersburg, Maryland U.S.A.) is used, following the conditions suggested by the manufacturer.

Normalized libraries are made using essentially the Soares procedure (Soares *et al., Proc. Natl. Acad. Sci. (U.S.A.) 91:*9228-9232 (1994), the entirety of which is herein incorporated by reference). This approach is designed to reduce the initial 10,000-fold variation in individual

15   cDNA frequencies to achieve abundances within one order of magnitude while maintaining the overall sequence complexity of the library. In the normalization process, the prevalence of high-abundance cDNA clones decreases dramatically, clones with mid-level abundance are relatively unaffected and clones for rare transcripts are effectively increased in abundance.

Normalized libraries are prepared from single-stranded and double-stranded DNA.

20   Single-stranded and double-stranded DNA representing approximately 1 X 10^6 colony forming units are isolated using standard protocols. RNA, complementary to the single-stranded DNA, is synthesized using the double stranded DNA as a template. Biotinylated dATP is incorporated

into the RNA during the synthesis reaction. The single-stranded DNA is mixed with the biotinylated RNA in a 1:10 molar ratio) and allowed to hybridize. DNA-RNA hybrids are captured on Dynabeads M280 streptavidin (Dynabeads, Dynal Corporation, Lake Success, New York U.S.A.). The dynabeads with captured hybrids are collected with a magnet. The non-

5 hybridized single-stranded molecules remaining after hybrid capture are converted to double stranded form and represent the primary normalized library.

For subtraction, target cDNA is made from the drought stressed tissue total RNA using the SMART cDNA synthesis system from Clonetech (Clonetech Laboratories, Palo Alto, California U.S.A.). Driver first strand cDNA is covalently linked to Dynabeads following a

10 protocol similar to that described in the Dynal literature (Dynabeads, Dynal Corporation, Lake Success, New York U.S.A.). The target cDNA is then heat denatured and the second strand trapped using Dynabeads oligo-dT. The target second strand cDNA is then hybridized to the driver cDNA in 400µl 2X SSPE for two rounds of hybridization at 65°C and 20 hours. After each hybridization, the hybridization solution is removed from the system and the hybridized

15 target cDNA removed from the driver by heat denaturation in water. After hybridization, the remaining cDNA is trapped with Dynabeads oligo-dT. The trapped cDNA is then amplified as in previous PCR based libraries and the resulting cDNA ligated into the pSPORT vector (Invitrogen, Carlsbad California U.S.A.).

Example 3

20 The cDNA libraries are plated on LB agar containing the appropriate antibiotics for selection and incubated at 37° for a sufficient time to allow the growth of individual colonies. Single colonies are individually placed in each well of a 96-well microtiter plates containing LB

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liquid including the selective antibiotics. The plates are incubated overnight at approximately 37°C with gentle shaking to promote growth of the cultures. The plasmid DNA is isolated from each clone using Qiaprep plasmid isolation kits, using the conditions recommended by the manufacturer (Qiagen Inc., Santa Clara, California U.S.A.).

5   Template plasmid DNA clones are used for subsequent sequencing. For sequencing, the ABI PRISM dRhodamine Terminator Cycle Sequencing Ready Reaction Kit with AmpliTaq® DNA Polymerase, FS, is used (PE Applied Biosystems, Foster City, California U.S.A.).

Example 4

Nucleic acid sequences that encode for the following phosphogluconate pathway enzymes: glucose-6-phosphate-1-dehydrogenase; 6-phosphogluconate dehydrogenase; putative 6-phosphogluconate dehydrogenase; D-ribulose-5-phosphate-3-epimerase; ribose-5-phosphate isomerase; putative ribose-5-phosphate isomerase; transketolase; putative transketolase; transaldolase; putative transaldolase; and phosphoglucoisomerase; are identified from the Monsanto EST PhytoSeq database using TBLASTN (default values)(TBLASTN compares a protein query against the six reading frames of a nucleic acid sequence). Matches found with BLAST P values equal or less than 0.001 (probability) or BLAST Score of equal or greater than 90 are classified as hits. If the program used to determine the hit is HMMSW then the score refers to HMMSW score.

In addition, the GenBank database is searched with BLASTN and BLASTX (default values) using ESTs as queries. EST that pass the hit probability threshold of $10e^{-8}$ for the following enzymes are combined with the hits generated by using TBLASTN (described above) and classified by enzyme (see Table A below).

A cluster refers to a set of overlapping clones in the PhytoSeq database. Such an overlapping relationship among clones is designated as a "cluster" when BLAST scores from pairwise sequence comparisons of the member clones meets a predetermined minimum value or product score of 50 or more (Product Score = (BLAST SCORE x Percentage Identity)/(5 x

5   minimum [length (Seq1), length (Seq2)])).

Since clusters are formed on the basis of single-linkage relationships, it is possible for two non-overlapping clones to be members of the same cluster if, for instance, they both overlap a third clone with at least the predetermined minimum BLAST score (stringency). A cluster ID is arbitrarily assigned to all of those clones which belong to the same cluster at a given

10   stringency and a particular clone will belong to only one cluster at a given stringency. If a cluster contains only a single clone (a "singleton"), then the cluster ID number will be negative, with an absolute value equal to the clone ID number of its single member. Clones grouped in a cluster in most cases represent a contiguous sequence.

IN THE UNITED STATES PATENT AND TRADEMARK OFFICE

In re application of:

Nordine CHEIKH *et al.*

Appln. No.: To Be Assigned

Filed: April 28, 1999

For: Nucleic Acid Molecules and Other Molecules Associated with the Phosphogluconate Pathway

Art Unit: To Be Assigned

Examiner: To Be Assigned

Atty. Docket: 04983.0031.US01/ 38-21(15365)B

Statement Regarding Sequence Submission

Assistant Commissioner for Patents
Washington, DC 20231

Sir:

In accordance with 37 C.F.R. § 1.821(f), the paper copy of the Sequence Listing and the computer readable copy of the Sequence Listing submitted herewith in the above-mentioned application are the same.

Respectfully submitted,
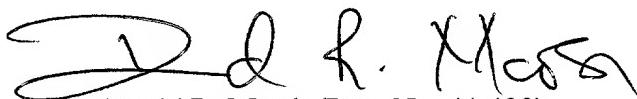
David R. Marsh (Reg. No. 41,408)

Date: April 28, 1999

HOWREY & SIMON
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TABLE A*

PHOSPHOGLUCONATE PATHWAY ENZYMES

MAIZE GLUCOSE-6-PHOSPHATE 1-DEHYDROGENASE

Seq No.	Cluster ID	CloneID	Library	NCBI gi	Method	Score	P-value	%Ident
1	-700047645	700047645H1	SATMON003	g471345	BLASTX	193	1e-21	58
2	-700210379	700210379H1	SATMON016	g1480344	BLASTX	103	1e-10	85
3	9135	700203121H1	SATMON003	g1166405	BLASTX	108	1e-10	78

SOYBEAN GLUCOSE-6-PHOSPHATE 1-DEHYDROGENASE

Seq No.	Cluster ID	CloneID	Library	NCBI gi	Method	Score	P-value	%Ident
4	-700869140	700869140H1	SOYMON016	g2829880	BLASTX	164	1e-15	44
5	-701065174	701065174H1	SOYMON034	g603219	BLASTX	86	1e-9	76
6	-701130434	701130434H1	SOYMON037	g1197385	BLASTX	189	1e-19	55
7	-701149522	701149522H1	SOYMON031	g603219	BLASTX	99	1e-8	71
8	26484	701003905H1	SOYMON019	g1197385	BLASTX	138	1e-15	81
9	9136	701038169H1	SOYMON029	g603219	BLASTX	139	1e-21	73
10	9136	700903571H1	SOYMON022	g603219	BLASTX	144	1e-20	81
11	9136	701045122H1	SOYMON032	g603219	BLASTX	100	1e-13	79

MAIZE 6-PHOSPHOGLUCONATE DEHYDROGENASE

Seq No.	Cluster ID	CloneID	Library	NCBI gi	Method	Score	P-value	%Ident
12	-L30686779	LIB3068-060-Q1-K1-G12	LIB3068	g603221	BLASTX	186	1e-34	78
13	416	LIB3066-006-Q1-K1-H7	LIB3066	g2529228	BLASTN	865	1e-63	72
14	4882	LIB3059-023-Q1-K1-E8	LIB3059	g2529228	BLASTN	1058	1e-79	72
15	4882	LIB3069-050-Q1-K1-H6	LIB3069	g2529229	BLASTX	252	1e-69	83
16	4882	LIB3066-024-Q1-K1-G4	LIB3066	g2529229	BLASTX	256	1e-60	79
17	4882	LIB143-002-Q1-E1-A7	LIB143	g2529228	BLASTN	794	1e-57	74
18	4882	LIB3069-043-Q1-K1-E1	LIB3069	g2529228	BLASTN	749	1e-52	73
19	4882	LIB189-026-Q1-E1-G9	LIB189	g2529228	BLASTN	566	1e-36	75
20	4882	LIB3069-054-Q1-K1-H7	LIB3069	g2529228	BLASTN	510	1e-31	75
21	4882	LIB3062-033-Q1-K1-B9	LIB3062	g603221	BLASTX	151	1e-29	70

SOYBEAN 6-PHOSPHOGLUCONATE DEHYDROGENASE

Seq No.	Cluster ID	CloneID	Library	NCBI gi	Method	Score	P-value	%Ident
22	-700660509	700660509H1	SOYMON004	g2529228	BLASTN	641	1e-58	82
23	-700851941	700851941H1	SOYMON023	g2529228	BLASTN	363	1e-20	94
24	-700988668	700988668H1	SOYMON009	g2529228	BLASTN	221	1e-27	99
25	-701065575	701065575H1	SOYMON034	g2529228	BLASTN	375	1e-20	95
26	-701097417	701097417H1	SOYMON028	g2529228	BLASTN	229	1e-20	90

27	-701097624	701097624H1	SOYMON028	g2529228	BLASTN	596	1e-40	70
28	-701108654	701108654H1	SOYMON036	g2529228	BLASTN	817	1e-59	85
29	-701127281	701127281H1	SOYMON037	g2529228	BLASTN	209	1e-8	90
30	1015	701136806H1	SOYMON038	g2529228	BLASTN	1221	1e-92	96
31	1015	701135971H1	SOYMON038	g2529228	BLASTN	971	1e-72	92
32	1015	700996470H1	SOYMON018	g2529228	BLASTN	940	1e-71	95
33	1015	700737338H1	SOYMON010	g2529228	BLASTN	469	1e-30	91
34	12395	700900348H1	SOYMON027	g2529228	BLASTN	1313	1e-100	97
35	12395	701099109H1	SOYMON028	g2529228	BLASTN	1252	1e-95	98
36	12395	701138412H1	SOYMON038	g2529228	BLASTN	1205	1e-91	95
37	12395	700995812H1	SOYMON011	g2529228	BLASTN	863	1e-85	95
38	12395	701097095H1	SOYMON028	g2529228	BLASTN	641	1e-84	95
39	12395	700667386H1	SOYMON006	g2529228	BLASTN	1082	1e-81	96
40	14379	701098379H1	SOYMON028	g2529228	BLASTN	1258	1e-96	99
41	14379	700667507H1	SOYMON006	g2529228	BLASTN	764	1e-54	94
42	14813	700790407H2	SOYMON011	g2529228	BLASTN	726	1e-60	82
43	14813	700790454H2	SOYMON011	g2529228	BLASTN	297	1e-43	84
44	23322	701056256H1	SOYMON032	g2529228	BLASTN	1079	1e-99	97
45	23322	701006115H1	SOYMON019	g2529228	BLASTN	828	1e-97	97
46	23322	701046496H1	SOYMON032	g2529228	BLASTN	753	1e-71	91
47	23322	701127189H1	SOYMON037	g2529228	BLASTN	440	1e-42	94
48	23861	701123687H1	SOYMON037	g2529228	BLASTN	995	1e-81	93
49	23861	700562186H1	SOYMON002	g2529228	BLASTN	787	1e-56	95
50	25330	701155571H1	SOYMON031	g2529228	BLASTN	922	1e-86	95
51	25330	701151123H1	SOYMON031	g2529228	BLASTN	1147	1e-86	99
52	25330	700869362H1	SOYMON016	g2529228	BLASTN	569	1e-75	94
53	2704	700651490H1	SOYMON003	g2529228	BLASTN	1482	1e-126	98
54	2704	700746336H1	SOYMON013	g2529228	BLASTN	1221	1e-105	99
55	2704	701127584H1	SOYMON037	g2529228	BLASTN	973	1e-100	97
56	2704	701062890H1	SOYMON033	g2529228	BLASTN	1173	1e-99	97
57	2704	701070368H1	SOYMON034	g2529228	BLASTN	686	1e-97	95
58	2704	700848709H1	SOYMON021	g2529228	BLASTN	1277	1e-97	98
59	2704	700904479H1	SOYMON022	g2529228	BLASTN	1281	1e-97	99
60	2704	700748881H1	SOYMON013	g2529228	BLASTN	1264	1e-96	96
61	2704	700746110H1	SOYMON013	g2529228	BLASTN	1257	1e-95	97
62	2704	701036989H1	SOYMON029	g2529228	BLASTN	1090	1e-94	95
63	2704	700986972H1	SOYMON009	g2529228	BLASTN	1173	1e-93	96
64	2704	700832482H1	SOYMON019	g2529228	BLASTN	1202	1e-93	98
65	2704	701209853H1	SOYMON035	g2529228	BLASTN	1210	1e-92	97
66	2704	700981060H1	SOYMON009	g2529228	BLASTN	1198	1e-91	93
67	2704	700730187H1	SOYMON009	g2529228	BLASTN	1182	1e-89	99
68	2704	701010566H1	SOYMON019	g2529228	BLASTN	649	1e-88	90
69	2704	701008609H1	SOYMON019	g2529228	BLASTN	1124	1e-88	91
70	2704	700727312H1	SOYMON009	g2529228	BLASTN	1171	1e-88	94
71	2704	700750187H1	SOYMON013	g2529228	BLASTN	1059	1e-84	94
72	2704	700747389H1	SOYMON013	g2529228	BLASTN	614	1e-82	92
73	2704	700988527H1	SOYMON009	g2529228	BLASTN	781	1e-81	92
74	2704	700836168H1	SOYMON019	g2529228	BLASTN	1079	1e-81	93
75	2704	700904775H1	SOYMON022	g2529228	BLASTN	491	1e-80	95
76	2704	700566794H1	SOYMON002	g2529228	BLASTN	1045	1e-78	96
77	2704	700764571H1	SOYMON022	g2529228	BLASTN	1028	1e-76	91
78	2704	701047371H1	SOYMON032	g2529228	BLASTN	995	1e-74	96
79	2704	700727986H1	SOYMON009	g2529228	BLASTN	619	1e-73	92
80	2704	701009981H2	SOYMON019	g2529228	BLASTN	840	1e-71	93

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81	2704	701049731H1	SOYMON032	g2529228	BLASTN	965	1e-71	98
82	2704	701105763H1	SOYMON036	g2529228	BLASTN	603	1e-70	92
83	2704	701214664H1	SOYMON035	g2529228	BLASTN	876	1e-64	93
84	2704	700889079H1	SOYMON024	g2529228	BLASTN	376	1e-43	92
85	2704	701037615H1	SOYMON029	g2529228	BLASTN	450	1e-28	85
86	502	700742139H1	SOYMON012	g2309076	BLASTX	179	1e-17	82
87	502	700743132H1	SOYMON012	g1573539	BLASTX	141	1e-12	87
88	6991	701048543H1	SOYMON032	g10409	BLASTX	116	1e-8	46
89	7306	700728579H1	SOYMON009	g2529228	BLASTN	797	1e-60	86
90	7306	700852657H1	SOYMON023	g2529228	BLASTN	739	1e-56	86
91	7306	700954712H1	SOYMON022	g2529228	BLASTN	700	1e-53	86
92	7306	700830929H1	SOYMON019	g2529228	BLASTN	693	1e-48	87
93	7306	700946027H1	SOYMON024	g2529228	BLASTN	681	1e-47	86
94	7306	701109643H1	SOYMON036	g2529228	BLASTN	566	1e-41	88
95	7306	700670024H1	SOYMON006	g2529228	BLASTN	478	1e-35	88
96	7306	700561367H1	SOYMON002	g2529228	BLASTN	274	1e-25	80
97	9847	700849887H1	SOYMON021	g2529228	BLASTN	246	1e-9	72
98	-GM11339	LIB3049-022-Q1-E1-H3	LIB3049	g2529228	BLASTN	1360	1e-111	86
99	14379	LIB3050-022-Q1-K1-H11	LIB3050	g2529228	BLASTN	1793	1e-143	96
100	14379	LIB3049-022-Q1-E1-H2	LIB3049	g2529228	BLASTN	1080	1e-137	97
101	16	LIB3040-004-Q1-E1-H4	LIB3040	g2529228	BLASTN	290	1e-36	96
102	23322	LIB3050-010-Q1-E1-D7	LIB3050	g2529228	BLASTN	726	1e-95	97
103	2704	LIB3039-020-Q1-E1-G6	LIB3039	g2529228	BLASTN	1060	1e-116	92

MAIZE PUTATIVE 6-PHOSPHOGLUCONATE DEHYDROGENASE

Seq No.	Cluster ID	CloneID	Library	NCBI gi	Method	Score	P-value	%Ident
104	-700159280	700159280H1	SATMON012	g3342801	BLASTN	677	1e-58	86
105	-700259383	700259383H1	SATMON017	g3342803	BLASTN	1210	1e-94	94
106	-700336103	700336103H1	SATMON019	g3342801	BLASTN	777	1e-93	96
107	-700347721	700347721H1	SATMON023	g3342799	BLASTN	282	1e-25	69
108	-700451974	700451974H1	SATMON028	g2529229	BLASTX	159	1e-15	60
109	-700549549	700549549H1	SATMON022	g3342799	BLASTN	1144	1e-86	86
110	-700570587	700570587H1	SATMON030	g3342801	BLASTN	780	1e-80	80
111	-701165285	701165285H1	SATMONN04	g3342801	BLASTN	469	1e-68	96
112	1485	700072738H1	SATMON007	g3342799	BLASTN	1670	1e-130	100
113	1485	700102916H1	SATMON010	g3342801	BLASTN	667	1e-107	97
114	1485	700075367H1	SATMON007	g3342799	BLASTN	1355	1e-104	100
115	1485	700215789H1	SATMON016	g3342799	BLASTN	1355	1e-104	100
116	1485	700618992H1	SATMON034	g3342799	BLASTN	926	1e-102	99
117	1485	700236444H1	SATMON010	g3342801	BLASTN	1237	1e-94	98
118	1485	701182383H1	SATMONN06	g3342801	BLASTN	707	1e-93	97
119	1485	700243716H1	SATMON010	g3342799	BLASTN	1233	1e-93	98
120	1485	700017132H1	SATMON001	g3342801	BLASTN	650	1e-84	100
121	1485	700000601H1	SATMON001	g3342801	BLASTN	1125	1e-84	100
122	1485	700000606H1	SATMON001	g3342801	BLASTN	1100	1e-82	100
123	1485	700473536H1	SATMON025	g3342799	BLASTN	1079	1e-81	97
124	1485	700000638H1	SATMON001	g3342801	BLASTN	1045	1e-78	100

125	1485	700000634H1	SATMON001	g3342801	BLASTN	1050	1e-78	100
126	1485	700000685H1	SATMON001	g3342801	BLASTN	1030	1e-77	100
127	1485	700620501H1	SATMON034	g3342801	BLASTN	834	1e-60	96
128	1485	700423115H1	SATMONN01	g3342801	BLASTN	718	1e-51	99
129	1485	700159096H1	SATMON012	g3342801	BLASTN	416	1e-48	84
130	1485	700450859H1	SATMON028	g3342799	BLASTN	414	1e-25	88
131	1485	700472336H1	SATMON025	g3342799	BLASTN	371	1e-22	90
132	17367	700615074H1	SATMON033	g3342802	BLASTX	120	1e-22	68
133	17367	700223083H1	SATMON011	g2529229	BLASTX	117	1e-18	58
134	20418	700142466H1	SATMON012	g3342801	BLASTN	586	1e-40	99
135	20418	700156495H1	SATMON012	g3342801	BLASTN	436	1e-27	97
136	416	700211273H1	SATMON016	g3342799	BLASTN	1536	1e-119	98
137	416	700085942H1	SATMON011	g3342799	BLASTN	1508	1e-116	99
138	416	700074747H1	SATMON007	g3342801	BLASTN	1018	1e-110	97
139	416	700572331H1	SATMON030	g3342799	BLASTN	1205	1e-108	98
140	416	700075257H1	SATMON007	g3342799	BLASTN	801	1e-105	98
141	416	700581966H1	SATMON031	g3342799	BLASTN	1330	1e-102	98
142	416	700220231H1	SATMON011	g3342801	BLASTN	1336	1e-102	99
143	416	700220126H1	SATMON011	g3342801	BLASTN	1327	1e-101	99
144	416	700238542H1	SATMON010	g3342801	BLASTN	1299	1e-99	98
145	416	700166459H1	SATMON013	g3342799	BLASTN	1217	1e-92	99
146	416	700221262H1	SATMON011	g3342801	BLASTN	1107	1e-83	90
147	416	700165558H1	SATMON013	g3342799	BLASTN	1061	1e-79	94
148	416	700449887H2	SATMON028	g3342799	BLASTN	986	1e-77	97
149	416	700460574H1	SATMON030	g3342799	BLASTN	702	1e-71	84
150	416	700220154H1	SATMON011	g3342801	BLASTN	917	1e-67	98
151	416	700614034H1	SATMON033	g3342799	BLASTN	666	1e-46	98
152	4839	700072438H2	SATMON007	g3342799	BLASTN	973	1e-103	96
153	4839	700021163H1	SATMON001	g3342799	BLASTN	853	1e-92	96
154	4839	700030139H1	SATMON003	g3342799	BLASTN	851	1e-91	98
155	4839	700021353H1	SATMON001	g3342799	BLASTN	866	1e-83	99
156	4839	700581184H1	SATMON031	g3342799	BLASTN	899	1e-73	95
157	4839	700219274H1	SATMON011	g3342801	BLASTN	518	1e-54	87
158	4839	700153705H1	SATMON007	g3342801	BLASTN	695	1e-52	87
159	4839	700341982H1	SATMON020	g3342799	BLASTN	360	1e-46	99
160	4839	700341234H1	SATMON020	g3342801	BLASTN	569	1e-38	89
161	4839	700343990H1	SATMON021	g3342799	BLASTN	366	1e-21	91
162	4882	700206482H1	SATMON003	g3342799	BLASTN	1592	1e-123	98
163	4882	700091812H1	SATMON011	g3342799	BLASTN	1546	1e-120	97
164	4882	700446652H1	SATMON027	g3342801	BLASTN	1455	1e-112	98
165	4882	700104823H1	SATMON010	g3342801	BLASTN	896	1e-111	98
166	4882	700356053H1	SATMON024	g3342801	BLASTN	1368	1e-105	97
167	4882	700219471H1	SATMON011	g3342801	BLASTN	920	1e-104	100
168	4882	700077133H1	SATMON007	g3342801	BLASTN	770	1e-102	97
169	4882	700208920H1	SATMON016	g3342801	BLASTN	701	1e-101	98
170	4882	700342808H1	SATMON021	g3342801	BLASTN	1170	1e-101	97
171	4882	700151209H1	SATMON007	g3342801	BLASTN	1321	1e-101	97
172	4882	700333146H1	SATMON019	g3342801	BLASTN	1011	1e-99	99
173	4882	700239943H1	SATMON010	g3342801	BLASTN	1295	1e-99	98
174	4882	700354623H1	SATMON024	g3342799	BLASTN	846	1e-98	98
175	4882	700348987H1	SATMON023	g3342801	BLASTN	997	1e-97	99
176	4882	700354655H1	SATMON024	g3342799	BLASTN	854	1e-94	96
177	4882	700075354H1	SATMON007	g3342801	BLASTN	1035	1e-93	100
178	4882	700351460H1	SATMON023	g3342801	BLASTN	946	1e-92	98

179	4882	700574482H1	SATMON030	g3342801	BLASTN	954	1e-92	97
180	4882	700455406H1	SATMON029	g3342801	BLASTN	663	1e-86	95
181	4882	700261343H1	SATMON017	g3342801	BLASTN	882	1e-81	93
182	4882	700156333H1	SATMON007	g3342801	BLASTN	1055	1e-79	100
183	4882	700152511H1	SATMON007	g3342801	BLASTN	786	1e-77	99
184	4882	700152557H1	SATMON007	g3342801	BLASTN	939	1e-74	97
185	4882	701176801H1	SATMONN05	g3342801	BLASTN	985	1e-73	100
186	4882	700242384H1	SATMON010	g3342801	BLASTN	676	1e-64	94
187	4882	700258317H1	SATMON017	g3342801	BLASTN	373	1e-61	98
188	4882	700377763H1	SATMON019	g3342801	BLASTN	615	1e-61	97
189	4882	700473877H1	SATMON025	g3342801	BLASTN	605	1e-46	100
190	4882	700076402H1	SATMON007	g3342801	BLASTN	256	1e-28	98
191	4882	700152333H1	SATMON007	g3342801	BLASTN	450	1e-28	100
192	4882	700155664H1	SATMON007	g3342801	BLASTN	260	1e-23	100
193	4882	700473648H1	SATMON025	g3342799	BLASTN	272	1e-16	91
194	4882	700548356H1	SATMON022	g3342799	BLASTN	290	1e-15	95
195	5830	700088306H1	SATMON011	g3342799	BLASTN	1604	1e-124	97
196	5830	700096066H1	SATMON008	g3342799	BLASTN	1575	1e-122	98
197	5830	700571406H1	SATMON030	g3342799	BLASTN	921	1e-118	96
198	5830	700075112H1	SATMON007	g3342799	BLASTN	1504	1e-116	95
199	5830	700050136H1	SATMON003	g3342799	BLASTN	1201	1e-91	97
200	5830	700028323H1	SATMON003	g3342799	BLASTN	1075	1e-90	97
201	5830	700076449H1	SATMON007	g3342799	BLASTN	1176	1e-89	94
202	5830	700352064H1	SATMON023	g3342799	BLASTN	1111	1e-86	96
203	5830	700346689H1	SATMON021	g3342799	BLASTN	1010	1e-75	96
204	5830	700217673H1	SATMON016	g3342799	BLASTN	1010	1e-75	97
205	5830	700350270H1	SATMON023	g3342799	BLASTN	405	1e-72	96
206	5830	700466829H1	SATMON025	g3342799	BLASTN	609	1e-50	96
207	5830	700220161H1	SATMON011	g3342799	BLASTN	590	1e-40	94
208	5830	700220192H1	SATMON011	g3342799	BLASTN	551	1e-37	96
209	5830	700453728H1	SATMON029	g3342799	BLASTN	491	1e-32	90

SOYBEAN PUTATIVE 6-PHOSPHOGLUCONATE DEHYDROGENASE

Seq No.	Cluster ID	CloneID	Library	NCBI gi	Method	Score	P-value	%Ident
210	17920	700889178H1	SOYMON024	g3342801	BLASTN	480	1e-30	71
211	17920	700976950H1	SOYMON009	g3342801	BLASTN	303	1e-16	67
212	489	700744939H1	SOYMON013	g3342804	BLASTX	250	1e-29	79
213	489	700748139H1	SOYMON013	g3342800	BLASTX	150	1e-27	65
214	5856	701070317H1	SOYMON034	g3342800	BLASTX	132	1e-21	73

MAIZE D-RIBULOSE-5-PHOSPHATE-3-EPIMERASE

Seq No.	Cluster ID	CloneID	Library	NCBI gi	Method	Score	P-value	%Ident
215	-700222465	700222465H1	SATMON011	g1162980	BLASTX	149	1e-27	84
216	-700618106	700618106H1	SATMON033	g902739	BLASTX	80	1e-25	76
217	10201	700101610H1	SATMON009	g902738	BLASTN	1009	1e-75	80
218	10201	700098237H1	SATMON009	g902738	BLASTN	1000	1e-74	80
219	10201	700209605H1	SATMON016	g1162979	BLASTN	976	1e-72	78
220	10201	700101988H1	SATMON009	g902738	BLASTN	626	1e-69	80
221	10201	700091966H1	SATMON011	g902738	BLASTN	905	1e-66	80
222	10201	700101445H1	SATMON009	g1162979	BLASTN	844	1e-61	80
223	10201	700159349H1	SATMON012	g902738	BLASTN	681	1e-48	73
224	10201	700380926H1	SATMON023	g902738	BLASTN	463	1e-45	81

225	17215	700048475H1	SATMON003	g1008313	BLASTX	177	1e-17	61
226	17215	700105805H1	SATMON010	g1008313	BLASTX	123	1e-10	59
227	1795	700432796H1	SATMONN01	g902739	BLASTX	139	1e-12	93
228	6043	700104089H1	SATMON010	g1162979	BLASTN	583	1e-39	79
229	6043	700099362H1	SATMON009	g1162980	BLASTX	156	1e-29	71
230	6043	700042321H1	SATMON004	g1162979	BLASTN	271	1e-27	79
231	6043	700457795H1	SATMON029	g902739	BLASTX	132	1e-25	64
232	6043	700096215H1	SATMON008	g1162980	BLASTX	120	1e-19	65
233	6043	700378379H1	SATMON019	g1162980	BLASTX	119	1e-17	86
234	6043	700239692H1	SATMON010	g1162980	BLASTX	167	1e-16	63
235	6043	700093535H1	SATMON008	g1162980	BLASTX	120	1e-13	61
236	6043	700098183H1	SATMON009	g1162980	BLASTX	121	1e-13	60
237	6043	700093175H1	SATMON008	g902739	BLASTX	126	1e-12	59
238	6043	700098056H1	SATMON009	g1162980	BLASTX	120	1e-9	57
239	6043	700101650H1	SATMON009	g1162980	BLASTX	120	1e-9	57
240	6043	700053356H1	SATMON009	g1162980	BLASTX	121	1e-9	57
241	6043	700099441H1	SATMON009	g902739	BLASTX	122	1e-9	58
242	7043	700162921H1	SATMON013	g1008313	BLASTX	130	1e-17	60
243	7043	700552657H1	SATMON022	g902739	BLASTX	154	1e-16	51
244	-L1891463	LIB189-001-Q1-E1-F4	LIB189	g1162979	BLASTN	596	1e-39	78
245	-L30781313	LIB3078-002-Q1-K1-A2	LIB3078	g1162979	BLASTN	440	1e-25	79
246	10201	LIB3078-034-Q1-K1-E8	LIB3078	g1162979	BLASTN	1271	1e-97	78
247	10201	LIB189-018-Q1-E1-G1	LIB189	g902738	BLASTN	1263	1e-96	79
248	10201	LIB3060-022-Q1-K1-G2	LIB3060	g902738	BLASTN	1228	1e-93	76
249	10201	LIB3060-034-Q1-K1-D3	LIB3060	g902738	BLASTN	1205	1e-91	79
250	10201	LIB36-007-Q1-E1-D10	LIB36	g1162979	BLASTN	989	1e-83	78
251	10201	LIB3078-053-Q1-K1-F4	LIB3078	g1162979	BLASTN	850	1e-62	68
252	10201	LIB189-034-Q1-E1-B12	LIB189	g902738	BLASTN	761	1e-53	74
253	1795	LIB3067-056-Q1-K1-A4	LIB3067	g902738	BLASTN	645	1e-43	80
254	6043	LIB189-017-Q1-E1-F12	LIB189	g1162979	BLASTN	842	1e-61	78
255	6043	LIB36-012-Q1-E1-H11	LIB36	g1162979	BLASTN	742	1e-51	78
256	6043	LIB3060-018-Q1-K1-B5	LIB3060	g1162979	BLASTN	653	1e-43	77
257	6043	LIB3062-015-Q1-K1-A11	LIB3062	g1162979	BLASTN	637	1e-42	77
258	6043	LIB189-031-Q1-E1-D1	LIB189	g1162979	BLASTN	532	1e-33	76
259	6043	LIB3060-013-Q1-K1-A2	LIB3060	g1162979	BLASTN	466	1e-27	75
260	7043	LIB148-032-Q1-E1-A4	LIB148	g2564973	BLASTX	238	1e-42	48

SOYBEAN D-RIBULOSE-5-PHOSPHATE-3-EPIMERASE

Seq No.	Cluster ID	CloneID	Library	NCBI gi	Method	Score	P-value	%Ident
261	-700677209	700677209H1	SOYMON007	g1162980	BLASTX	130	1e-30	85
262	10469	700971857H1	SOYMON005	g1008313	BLASTX	208	1e-27	55
263	10469	701064495H1	SOYMON034	g1008313	BLASTX	208	1e-27	56
264	10469	701007767H1	SOYMON019	g1008313	BLASTX	129	1e-25	54
265	10469	700656367H1	SOYMON004	g1008313	BLASTX	182	1e-22	57
266	15209	700791582H1	SOYMON011	g2388956	BLASTX	129	1e-10	66
267	15209	701001180H1	SOYMON018	g1008313	BLASTX	122	1e-9	65
268	18337	700739263H1	SOYMON012	g902738	BLASTN	481	1e-50	82
269	18337	700681545H1	SOYMON008	g1162979	BLASTN	342	1e-44	83
270	18818	700866167H1	SOYMON016	g1162979	BLASTN	853	1e-62	89
271	18818	700983968H1	SOYMON009	g1162979	BLASTN	422	1e-55	76
272	5784	700999796H1	SOYMON018	g1162979	BLASTN	535	1e-43	78
273	5784	700788240H1	SOYMON011	g902738	BLASTN	455	1e-36	77
274	5784	701000905H1	SOYMON018	g902738	BLASTN	501	1e-36	77
275	5784	701040171H1	SOYMON029	g902738	BLASTN	510	1e-33	78
276	5784	700754807H1	SOYMON014	g902738	BLASTN	447	1e-31	72
277	5784	700904930H1	SOYMON022	g902738	BLASTN	465	1e-29	77
278	5784	700739828H1	SOYMON012	g902738	BLASTN	455	1e-28	76
279	5784	700741008H1	SOYMON012	g1162980	BLASTX	142	1e-16	81
280	5784	700738184H1	SOYMON012	g1162980	BLASTX	167	1e-16	81
281	5784	700790753H1	SOYMON011	g1162980	BLASTX	149	1e-15	79
282	5784	701110183H1	SOYMON036	g1162980	BLASTX	161	1e-15	81
283	5784	700876264H1	SOYMON018	g1162980	BLASTX	140	1e-12	87
284	5784	700787492H2	SOYMON011	g1162980	BLASTX	141	1e-12	76
285	5784	700788242H1	SOYMON011	g1162980	BLASTX	80	1e-11	89
286	5784	700741612H1	SOYMON012	g1162980	BLASTX	103	1e-11	78
287	5784	700789926H2	SOYMON011	g1162980	BLASTX	119	1e-11	74
288	5784	701105542H1	SOYMON036	g1162980	BLASTX	117	1e-10	66
289	5784	700741161H1	SOYMON012	g1162980	BLASTX	101	1e-8	63
290	5784	700877044H1	SOYMON018	g902738	BLASTN	236	1e-8	73
291	9624	700659817H1	SOYMON004	g1162979	BLASTN	959	1e-71	85
292	9624	700558457H1	SOYMON001	g1162979	BLASTN	533	1e-64	81
293	9624	700898624H1	SOYMON027	g1162979	BLASTN	867	1e-63	83
294	9624	700848716H1	SOYMON021	g1162979	BLASTN	680	1e-61	83
295	9624	700990488H1	SOYMON011	g1162979	BLASTN	763	1e-54	83
296	9624	700980873H1	SOYMON009	g1162979	BLASTN	722	1e-51	77
297	9624	700654880H1	SOYMON004	g1162979	BLASTN	473	1e-36	71
298	10469	LIB3040-057-Q1-E1-C5	LIB3040	g1008313	BLASTX	205	1e-60	54
299	9624	LIB3030-001-Q1-B1-F10	LIB3030	g1162979	BLASTN	1185	1e-90	80

MAIZE RIBOSE-5-PHOSPHATE ISOMERASE

Seq No.	Cluster ID	CloneID	Library	NCBI gi	Method	Score	P-value	%Ident
300	5053	700206243H1	SATMON003	g1669358	BLASTX	165	1e-20	59
301	5053	700157368H1	SATMON012	g1001678	BLASTX	188	1e-19	59
302	-L30672312	LIB3067-007-Q1-K1-C3	LIB3067	g1789280	BLASTX	114	1e-24	54
303	-L841459	LIB84-028-Q1-E1-A11	LIB84	g1789280	BLASTX	117	1e-25	53
304	5053	LIB3078-033-	LIB3078	g1001678	BLASTX	217	1e-42	50

		Q1-K1-A2						
305	5053	LIB3060-054-Q1-K1-G1	LIB3060	g2649655	BLASTX	100	1e-34	48
306	5053	LIB3078-054-Q1-K1-B9	LIB3078	g1669358	BLASTX	65	1e-24	40

SOYBEAN RIBOSE-5-PHOSPHATE ISOMERASE

Seq No.	Cluster ID	CloneID	Library	NCBI gi	Method	Score	P-value	%Ident
307	17047	700737894H1	SOYMON012	g1001678	BLASTX	93	1e-14	62
308	17047	700790677H2	SOYMON011	g2649655	BLASTX	68	1e-9	47
309	17047	700891079H1	SOYMON024	g1001678	BLASTX	122	1e-9	56
310	8783	701120985H1	SOYMON037	g1789280	BLASTX	115	1e-9	51
311	8783	700745725H1	SOYMON013	g1789280	BLASTX	113	1e-8	51

MAIZE PUTATIVE RIBOSE-5-PHOSPHATE ISOMERASE

Seq No.	Cluster ID	CloneID	Library	NCBI gi	Method	Score	P-value	%Ident
312	-700622640	700622640H1	SATMON034	g3257798	BLASTX	128	1e-10	63
313	5053	700213140H1	SATMON016	g500774	BLASTX	195	1e-20	43

SOYBEAN PUTATIVE RIBOSE-5-PHOSPHATE ISOMERASE

Seq No.	Cluster ID	CloneID	Library	NCBI gi	Method	Score	P-value	%Ident
314	-700840778	700840778H1	SOYMON020	g500774	BLASTX	203	1e-21	51
315	-700898355	700898355H1	SOYMON027	g3257798	BLASTX	108	1e-17	60
316	16333	700562390H1	SOYMON002	g500774	BLASTX	211	1e-22	44
317	16333	700961206H1	SOYMON022	g500774	BLASTX	145	1e-14	51
318	8873	701120413H1	SOYMON037	g3257798	BLASTX	134	1e-11	48

MAIZE TRANSKETOLASE

Seq No.	Cluster ID	CloneID	Library	NCBI gi	Method	Score	P-value	%Ident
319	-700097383	700097383H1	SATMON009	g664902	BLASTN	1029	1e-76	80
320	-701159054	701159054H1	SATMONN04	g2529342	BLASTX	214	1e-27	79
321	-701184582	701184582H1	SATMONN06	g1658321	BLASTN	745	1e-53	74
322	1244	700553205H1	SATMON022	g1658321	BLASTN	816	1e-59	75
323	1244	700473792H1	SATMON025	g1658321	BLASTN	826	1e-59	75
324	1244	700405168H1	SATMON028	g1658321	BLASTN	805	1e-58	75
325	1244	700089307H1	SATMON011	g1658321	BLASTN	743	1e-53	74
326	1244	700355533H1	SATMON024	g1658321	BLASTN	589	1e-51	76
327	1244	700085136H1	SATMON011	g1658321	BLASTN	690	1e-48	76
328	1244	700382850H1	SATMON024	g664900	BLASTN	537	1e-47	72
329	1244	700454437H1	SATMON029	g1658321	BLASTN	655	1e-45	75
330	1244	700150022H1	SATMON007	g1658321	BLASTN	606	1e-41	76
331	1244	700212701H1	SATMON016	g1658321	BLASTN	507	1e-40	74
332	1244	700438654H1	SATMON026	g2529342	BLASTX	160	1e-24	89
333	1244	700458530H1	SATMON029	g2529342	BLASTX	177	1e-20	87
334	2946	700262031H1	SATMON017	g1658321	BLASTN	467	1e-30	74
335	3403	700075930H1	SATMON007	g664900	BLASTN	968	1e-71	81
336	3403	700381012H1	SATMON023	g1658321	BLASTN	949	1e-70	80
337	3403	700243701H1	SATMON010	g1658321	BLASTN	874	1e-63	80
338	3403	700220485H1	SATMON011	g664900	BLASTN	666	1e-54	74
339	3403	700045165H1	SATMON004	g664900	BLASTN	734	1e-52	73
340	3403	701185190H1	SATMONN06	g664900	BLASTN	709	1e-50	77

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341	3403	700552475H1	SATMON022	g664900	BLASTN	591	1e-49	81
342	3403	700044755H1	SATMON004	g664900	BLASTN	690	1e-48	72
343	3403	700051910H1	SATMON003	g664900	BLASTN	671	1e-47	77
344	3403	700027425H1	SATMON003	g664900	BLASTN	675	1e-47	71
345	3403	700048347H1	SATMON003	g664900	BLASTN	662	1e-46	71
346	3403	700380608H1	SATMON021	g1658321	BLASTN	623	1e-43	82
347	3403	700448484H1	SATMON027	g664900	BLASTN	522	1e-33	71
348	3403	700184906H1	SATMON014	g2529342	BLASTX	251	1e-27	77
349	3403	700048819H1	SATMON003	g664900	BLASTN	453	1e-27	74
350	3403	701167994H1	SATMONN05	g2529342	BLASTX	193	1e-19	76
351	8097	700084375H1	SATMON011	g664900	BLASTN	855	1e-76	79
352	8097	700445226H1	SATMON027	g664900	BLASTN	464	1e-60	79
353	8097	700240770H1	SATMON010	g664900	BLASTN	750	1e-60	80
354	8097	700045122H1	SATMON004	g664900	BLASTN	638	1e-54	80
355	3403	LIB3060-013-Q1-K1-A12	LIB3060	g664900	BLASTN	1052	1e-78	72
356	3403	LIB3078-007-Q1-K1-G3	LIB3078	g664900	BLASTN	629	1e-41	69

SOYBEAN TRANSKETOLASE

Seq No.	Cluster ID	CloneID	Library	NCBI gi	Method	Score	P-value	%Ident
357	-700646481	700646481H1	SOYMON013	g1658321	BLASTN	967	1e-71	83
358	-700734535	700734535H1	SOYMON010	g1658321	BLASTN	822	1e-59	82
359	-700865886	700865886H1	SOYMON016	g1658321	BLASTN	568	1e-38	82
360	-700943688	700943688H1	SOYMON024	g1658321	BLASTN	902	1e-66	82
361	-700954594	700954594H1	SOYMON022	g2529342	BLASTX	172	1e-16	75
362	-701064360	701064360H1	SOYMON034	g664901	BLASTX	179	1e-17	80
363	1039	700662776H1	SOYMON005	g1658321	BLASTN	755	1e-78	83
364	1039	700663764H1	SOYMON005	g1658321	BLASTN	839	1e-61	82
365	1039	700952282H1	SOYMON022	g1658321	BLASTN	785	1e-56	81
366	1039	700835426H1	SOYMON019	g1658321	BLASTN	748	1e-53	81
367	1039	700738038H1	SOYMON012	g1658321	BLASTN	559	1e-37	80
368	1040	700606230H1	SOYMON008	g1658321	BLASTN	532	1e-69	82
369	1040	700681196H2	SOYMON008	g1658321	BLASTN	866	1e-63	80
370	1040	700876408H1	SOYMON018	g1658321	BLASTN	475	1e-60	82
371	1040	700901259H1	SOYMON027	g1658321	BLASTN	821	1e-59	81
372	1040	700996991H1	SOYMON018	g1658321	BLASTN	450	1e-58	80
373	1040	700876984H1	SOYMON018	g1658321	BLASTN	807	1e-58	81
374	1040	700871885H1	SOYMON018	g1658321	BLASTN	812	1e-58	81
375	1040	700740158H1	SOYMON012	g1658321	BLASTN	767	1e-55	78
376	1040	700787592H1	SOYMON011	g1658321	BLASTN	770	1e-55	80
377	1040	700789355H2	SOYMON011	g1658321	BLASTN	727	1e-51	81
378	1040	700786173H2	SOYMON011	g1658321	BLASTN	523	1e-47	79
379	1040	700987027H1	SOYMON009	g1658321	BLASTN	680	1e-47	78
380	1040	700683335H1	SOYMON008	g1658321	BLASTN	567	1e-38	80
381	1040	700742402H1	SOYMON012	g1658321	BLASTN	521	1e-34	78
382	1040	700682934H1	SOYMON008	g1658322	BLASTX	111	1e-22	79
383	1040	701001535H1	SOYMON018	g664900	BLASTN	337	1e-18	85
384	1381	701002017H1	SOYMON018	g1658321	BLASTN	860	1e-62	81
385	1381	700680946H1	SOYMON008	g1658321	BLASTN	848	1e-61	75
386	1381	700785920H2	SOYMON011	g1658321	BLASTN	715	1e-60	80
387	1381	700741325H1	SOYMON012	g1658321	BLASTN	836	1e-60	81
388	1381	700737257H1	SOYMON010	g1658321	BLASTN	783	1e-56	83

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389	1381	700743637H1	SOYMON012	g1658321	BLASTN	456	1e-47	79
390	1381	700683536H1	SOYMON008	g1658321	BLASTN	682	1e-47	82
391	1381	700899577H1	SOYMON027	g1658321	BLASTN	632	1e-43	73
392	1381	700655539H1	SOYMON004	g1658321	BLASTN	399	1e-32	77
393	1381	700743117H1	SOYMON012	g664901	BLASTX	144	1e-12	88
394	1381	701047167H1	SOYMON032	g1658321	BLASTN	147	1e-10	88
395	1694	700557862H1	SOYMON001	g1658321	BLASTN	918	1e-67	81
396	1694	701124388H1	SOYMON037	g1658321	BLASTN	884	1e-64	84
397	1694	700977906H1	SOYMON009	g1658321	BLASTN	741	1e-60	81
398	1694	700741633H1	SOYMON012	g1658321	BLASTN	753	1e-60	83
399	20534	701214424H1	SOYMON035	g1658321	BLASTN	855	1e-62	80
400	20534	701214345H1	SOYMON035	g1658321	BLASTN	845	1e-61	81
401	20534	700737144H1	SOYMON010	g1658321	BLASTN	743	1e-53	79
402	20534	700737045H1	SOYMON010	g1658321	BLASTN	716	1e-50	80
403	2081	700684191H1	SOYMON008	g1658321	BLASTN	243	1e-11	68
404	2081	700871634H1	SOYMON018	g1658321	BLASTN	243	1e-9	65
405	2081	700896859H1	SOYMON027	g1658321	BLASTN	243	1e-9	65
406	2081	700741968H1	SOYMON012	g1658321	BLASTN	243	1e-9	65
407	2081	700743285H1	SOYMON012	g1658321	BLASTN	234	1e-8	65
408	2081	701105794H1	SOYMON036	g1658321	BLASTN	236	1e-8	65
409	2081	700646243H1	SOYMON012	g1658321	BLASTN	236	1e-8	65
410	2081	701104160H1	SOYMON036	g1658321	BLASTN	236	1e-8	65
411	2081	700741863H1	SOYMON012	g1658321	BLASTN	238	1e-8	65
412	2091	700651076H1	SOYMON003	g1658321	BLASTN	1055	1e-79	79
413	2091	700874803H1	SOYMON018	g1658321	BLASTN	888	1e-65	82
414	2091	700988611H1	SOYMON009	g1658321	BLASTN	419	1e-61	79
415	2091	700657810H1	SOYMON004	g1658321	BLASTN	805	1e-58	81
416	2091	700739094H1	SOYMON012	g1658321	BLASTN	425	1e-54	82
417	2091	700962626H1	SOYMON022	g1658321	BLASTN	742	1e-52	78
418	2091	700990046H1	SOYMON011	g1658321	BLASTN	376	1e-34	79
419	3782	700870543H1	SOYMON018	g1658322	BLASTX	157	1e-25	68
420	4096	700556949H1	SOYMON001	g664901	BLASTX	188	1e-18	92
421	4096	700877014H1	SOYMON018	g664901	BLASTX	188	1e-18	92
422	4096	700877022H1	SOYMON018	g664901	BLASTX	188	1e-18	92
423	4096	700999039H1	SOYMON018	g664901	BLASTX	169	1e-16	91
424	7870	700998419H1	SOYMON018	g1658321	BLASTN	430	1e-51	80
425	7870	700557019H1	SOYMON001	g1658321	BLASTN	685	1e-48	80
426	7870	700786020H2	SOYMON011	g1658321	BLASTN	531	1e-41	78
427	7870	700740475H1	SOYMON012	g1658321	BLASTN	609	1e-41	74
428	7870	700875020H1	SOYMON018	g1658321	BLASTN	525	1e-34	79
429	7870	700674249H1	SOYMON007	g1658321	BLASTN	510	1e-33	82
430	7870	700658256H1	SOYMON004	g2529342	BLASTX	178	1e-22	61
431	7870	700677401H1	SOYMON007	g664901	BLASTX	158	1e-14	91
432	9031	700874020H1	SOYMON018	g1658321	BLASTN	789	1e-56	79
433	9031	700726463H1	SOYMON009	g1658321	BLASTN	758	1e-54	76
434	9031	700869017H1	SOYMON016	g664900	BLASTN	743	1e-53	77
435	9031	700566216H1	SOYMON002	g664901	BLASTX	201	1e-20	92
436	1039	LIB3051-053-Q1-K2-F1	LIB3051	g1658321	BLASTN	1326	1e-101	80
437	9031	LIB3039-045-Q1-E1-D1	LIB3039	g1658321	BLASTN	1033	1e-77	79

MAIZE PUTATIVE TRANSKETOLASE

Seq No.	Cluster ID	CloneID	Library	NCBI gi	Method	Score	P-value	%Ident
438	-700045462	700045462H1	SATMON004	g2612940	BLASTN	1219	1e-92	89
439	-700223919	700223919H1	SATMON011	g2612940	BLASTN	1025	1e-76	87
440	-700256830	700256830H1	SATMON017	g2612940	BLASTN	1029	1e-76	87
441	-701169515	701169515H1	SATMONN05	g2612940	BLASTN	327	1e-40	92
442	23377	700263420H1	SATMON017	g2612940	BLASTN	489	1e-31	75
443	23377	701185311H1	SATMONN06	g2612940	BLASTN	460	1e-27	78
444	7446	700624329H1	SATMON034	g2612940	BLASTN	1046	1e-87	88
445	7446	700159091H1	SATMON012	g2612940	BLASTN	898	1e-77	89
446	-L30626416	LIB3062-048-Q1-K1-D12	LIB3062	g2612940	BLASTN	808	1e-74	86
447	-L30684293	LIB3068-046-Q1-K1-B2	LIB3068	g2612940	BLASTN	846	1e-90	87

SOYBEAN PUTATIVE TRANSKETOLASE

Seq No.	Cluster ID	CloneID	Library	NCBI gi	Method	Score	P-value	%Ident
448	19183	700907766H1	SOYMON022	g2612940	BLASTN	395	1e-30	68
449	-700764341	700764341H1	SOYMON021	g2612941	BLASTX	247	1e-39	75
450	-700888745	700888745H1	SOYMON024	g2612941	BLASTX	237	1e-27	76
451	-700909473	700909473H1	SOYMON022	g2612941	BLASTX	114	1e-16	53
452	7224	700681472H2	SOYMON008	g2612941	BLASTX	107	1e-12	72
453	19325	700751059H1	SOYMON014	g2244912	BLASTX	160	1e-15	78

MAIZE TRANSALDOLASE

Seq No.	Cluster ID	CloneID	Library	NCBI gi	Method	Score	P-value	%Ident
454	-700074081	700074081H1	SATMON007	g2078350	BLASTX	199	1e-26	79
455	-700087740	700087740H1	SATMON011	g2078349	BLASTN	651	1e-45	68
456	10709	700049020H1	SATMON003	g2078350	BLASTX	131	1e-10	67
457	143	700207653H1	SATMON016	g2078349	BLASTN	911	1e-67	76
458	143	700099852H1	SATMON009	g2078349	BLASTN	889	1e-65	75
459	143	700268119H1	SATMON017	g2078349	BLASTN	872	1e-63	76
460	143	700211193H1	SATMON016	g2078349	BLASTN	848	1e-61	76
461	143	700454251H1	SATMON029	g2078349	BLASTN	829	1e-60	78
462	143	700204216H1	SATMON003	g2078349	BLASTN	801	1e-57	76
463	143	700333262H1	SATMON019	g2078349	BLASTN	691	1e-56	74
464	143	700618845H1	SATMON034	g2078349	BLASTN	781	1e-56	76
465	143	700239238H1	SATMON010	g2078349	BLASTN	776	1e-55	76
466	143	700205539H1	SATMON003	g2078349	BLASTN	754	1e-54	73
467	143	700344192H1	SATMON021	g2078349	BLASTN	756	1e-54	75
468	143	700239126H1	SATMON010	g2078349	BLASTN	733	1e-52	73
469	143	700207418H1	SATMON016	g2078349	BLASTN	736	1e-52	70
470	143	700575204H1	SATMON030	g2078349	BLASTN	741	1e-52	71
471	143	700442682H1	SATMON026	g2078349	BLASTN	725	1e-51	74
472	143	700343686H1	SATMON021	g2078349	BLASTN	556	1e-49	74
473	143	700241386H1	SATMON010	g2078349	BLASTN	694	1e-49	75
474	143	700209193H1	SATMON016	g2078349	BLASTN	704	1e-49	72
475	143	700549360H1	SATMON022	g2078349	BLASTN	689	1e-48	77
476	143	700213668H1	SATMON016	g2078349	BLASTN	690	1e-48	72
477	143	700099381H1	SATMON009	g2078349	BLASTN	691	1e-48	73
478	143	700241472H1	SATMON010	g2078349	BLASTN	507	1e-47	76
479	143	700158253H1	SATMON012	g2078349	BLASTN	670	1e-47	76

480	143	700243043H1	SATMON010	g2078349	BLASTN	680	1e-47	73
481	143	700077153H1	SATMON007	g2078350	BLASTX	238	1e-46	74
482	143	700094547H1	SATMON008	g2078349	BLASTN	659	1e-46	73
483	143	700237891H1	SATMON010	g2078349	BLASTN	638	1e-44	71
484	143	700142446H1	SATMON012	g2078349	BLASTN	625	1e-43	75
485	143	700440545H1	SATMON026	g2078349	BLASTN	626	1e-43	71
486	143	700622336H1	SATMON034	g2078349	BLASTN	633	1e-43	72
487	143	700082380H1	SATMON011	g2078349	BLASTN	610	1e-42	70
488	143	700171422H1	SATMON013	g2078349	BLASTN	602	1e-41	77
489	143	700449973H1	SATMON028	g2078349	BLASTN	609	1e-41	70
490	143	701182293H1	SATMONN06	g2078349	BLASTN	480	1e-40	72
491	143	700154086H1	SATMON007	g2078349	BLASTN	592	1e-40	71
492	143	700018427H1	SATMON001	g2078349	BLASTN	593	1e-40	78
493	143	700615631H1	SATMON033	g2078349	BLASTN	608	1e-40	71
494	143	700550235H1	SATMON022	g2078350	BLASTX	237	1e-38	78
495	143	700203959H1	SATMON003	g2078349	BLASTN	571	1e-38	73
496	143	700152039H1	SATMON007	g2078349	BLASTN	532	1e-35	72
497	143	700207472H1	SATMON016	g2078350	BLASTX	168	1e-34	67
498	143	700580755H1	SATMON031	g2078350	BLASTX	202	1e-33	73
499	143	700477590H1	SATMON025	g2078349	BLASTN	365	1e-32	74
500	143	700083979H1	SATMON011	g2078349	BLASTN	517	1e-32	70
501	143	700569751H1	SATMON030	g2078350	BLASTX	161	1e-30	63
502	143	700239239H1	SATMON010	g2078350	BLASTX	182	1e-30	69
503	143	700469525H1	SATMON025	g2078350	BLASTX	270	1e-30	64
504	143	700242890H1	SATMON010	g2078349	BLASTN	451	1e-28	71
505	143	700168126H1	SATMON013	g2078349	BLASTN	448	1e-27	71
506	143	700338361H1	SATMON020	g2078349	BLASTN	441	1e-26	72
507	143	700337834H1	SATMON020	g2078349	BLASTN	444	1e-26	73
508	143	700339742H1	SATMON020	g2078349	BLASTN	434	1e-25	71
509	143	700205161H1	SATMON003	g2078350	BLASTX	171	1e-22	69
510	143	700171567H1	SATMON013	g2078350	BLASTX	212	1e-21	86
511	143	700202495H1	SATMON003	g2078350	BLASTX	195	1e-19	80
512	143	700266495H1	SATMON017	g2078350	BLASTX	175	1e-16	73
513	143	701173375H2	SATMONN05	g2078350	BLASTX	112	1e-13	78
514	143	700404964H1	SATMON027	g2078350	BLASTX	133	1e-11	77
515	143	700430542H1	SATMONN01	g2078350	BLASTX	137	1e-11	77
516	143	701181429H1	SATMONN06	g2078349	BLASTN	238	1e-8	74
517	14658	700622708H1	SATMON034	g4602	BLASTX	144	1e-20	40
518	14658	700196413H1	SATMON014	g1574680	BLASTX	118	1e-9	43
519	15681	700261694H1	SATMON017	g4602	BLASTX	80	1e-10	35
520	143	LIB3062-030-Q1-K1-A8	LIB3062	g2078349	BLASTN	878	1e-80	74
521	143	LIB3060-017-Q1-K1-G11	LIB3060	g2078349	BLASTN	1041	1e-77	73
522	143	LIB3060-002-Q1-K2-A11	LIB3060	g2078349	BLASTN	1009	1e-75	73
523	143	LIB3069-030-Q1-K1-A11	LIB3069	g2078349	BLASTN	877	1e-68	71
524	143	LIB3060-032-Q1-K1-C7	LIB3060	g2078349	BLASTN	660	1e-66	72
525	143	LIB3059-017-Q1-K1-B4	LIB3059	g2078349	BLASTN	885	1e-64	73
526	143	LIB3066-053-Q1-K1-G10	LIB3066	g2078349	BLASTN	833	1e-60	69

527	143	LIB3060-017-Q1-K1-G12	LIB3060	g2078349	BLASTN	756	1e-53	73
528	143	LIB143-027-Q1-E1-B11	LIB143	g2078350	BLASTX	246	1e-42	75
529	143	LIB3059-016-Q1-K1-H12	LIB3059	g2078350	BLASTX	138	1e-36	59
530	15681	LIB3062-027-Q1-K1-H4	LIB3062	g1786189	BLASTX	112	1e-32	42
531	19642	LIB143-006-Q1-E1-H7	LIB143	g1574680	BLASTX	91	1e-26	41
532	29728	LIB3079-007-Q1-K1-G3	LIB3079	g2078350	BLASTX	238	1e-41	68
533	29728	LIB3069-033-Q1-K1-E2	LIB3069	g2078350	BLASTX	96	1e-25	65

SOYBEAN TRANSALDOLASE

Seq No.	Cluster ID	CloneID	Library	NCBI gi	Method	Score	P-value	%Ident
534	-700557848	700557848H1	SOYMON001	g1786189	BLASTX	138	1e-12	62
535	-700898220	700898220H1	SOYMON027	g2078350	BLASTX	96	1e-13	79
536	-701053141	701053141H1	SOYMON032	g2078350	BLASTX	190	1e-24	63
537	12032	701209342H1	SOYMON035	g2078349	BLASTN	882	1e-64	79
538	12032	700566011H1	SOYMON002	g2078349	BLASTN	521	1e-43	79
539	12032	700957709H1	SOYMON022	g2078349	BLASTN	607	1e-41	72
540	16286	701014315H1	SOYMON019	g2078349	BLASTN	632	1e-43	75
541	16286	700733731H1	SOYMON010	g2078350	BLASTX	171	1e-27	64
542	16286	700978907H1	SOYMON009	g2078349	BLASTN	452	1e-27	75
543	16286	700675063H1	SOYMON007	g2078350	BLASTX	159	1e-23	66
544	18022	700963175H1	SOYMON022	g2078349	BLASTN	771	1e-55	80
545	18022	700892251H1	SOYMON024	g2078349	BLASTN	519	1e-34	81
546	18700	700741418H1	SOYMON012	g2078349	BLASTN	440	1e-26	75
547	18700	701210709H1	SOYMON035	g2078350	BLASTX	227	1e-24	90
548	18700	700867261H1	SOYMON016	g2078350	BLASTX	158	1e-14	85
549	18700	700867361H1	SOYMON016	g2078349	BLASTN	179	1e-11	79
550	3993	700893136H1	SOYMON024	g2078349	BLASTN	725	1e-51	78
551	3993	700747125H1	SOYMON013	g2078349	BLASTN	613	1e-49	79
552	3993	701044349H1	SOYMON032	g2078349	BLASTN	630	1e-43	74
553	3993	700832771H1	SOYMON019	g2078349	BLASTN	608	1e-41	74
554	3993	700975359H1	SOYMON009	g2078349	BLASTN	449	1e-28	71
555	3993	700970463H1	SOYMON005	g2078350	BLASTX	83	1e-22	74
556	3993	701012833H1	SOYMON019	g2078350	BLASTX	207	1e-21	52
557	3993	700794982H1	SOYMON017	g2078349	BLASTN	335	1e-19	75
558	3993	701012461H1	SOYMON019	g2078350	BLASTX	189	1e-18	50
559	3993	700982758H1	SOYMON009	g2078349	BLASTN	337	1e-17	75
560	3993	701102424H1	SOYMON028	g2078350	BLASTX	161	1e-15	70
561	3993	700746415H1	SOYMON013	g2078349	BLASTN	320	1e-15	74
562	3993	700897055H1	SOYMON027	g2078349	BLASTN	289	1e-13	73
563	3993	700967006H1	SOYMON029	g2078349	BLASTN	289	1e-13	73
564	3993	701100750H1	SOYMON028	g2078349	BLASTN	182	1e-12	78
565	3993	701055410H1	SOYMON032	g2078350	BLASTX	120	1e-11	60
566	3993	701040696H1	SOYMON029	g2078349	BLASTN	263	1e-11	72
567	3993	701211427H1	SOYMON035	g2078350	BLASTX	73	1e-10	50
568	3993	700963010H1	SOYMON022	g2078350	BLASTX	73	1e-10	50
569	3993	701099581H1	SOYMON028	g2078350	BLASTX	97	1e-10	50

570	3993	700888568H1	SOYMON024	g2078350	BLASTX	112	1e-10	47
571	3993	701011889H1	SOYMON019	g2078350	BLASTX	124	1e-10	48
572	3993	700726386H1	SOYMON009	g2078350	BLASTX	90	1e-9	48
573	3993	700943367H1	SOYMON024	g2078349	BLASTN	242	1e-9	72
574	3993	700650311H1	SOYMON003	g2078349	BLASTN	242	1e-9	72
575	3993	701008074H1	SOYMON019	g2078350	BLASTX	83	1e-8	48
576	3993	700955316H1	SOYMON022	g2078349	BLASTN	155	1e-8	72
577	3993	701043442H1	SOYMON029	g2078349	BLASTN	234	1e-8	73
578	3993	700905939H1	SOYMON022	g2078349	BLASTN	234	1e-8	73
579	3993	700728911H1	SOYMON009	g2078349	BLASTN	234	1e-8	73
580	4079	700565922H1	SOYMON002	g2078349	BLASTN	574	1e-72	83
581	4079	700991339H1	SOYMON011	g2078349	BLASTN	918	1e-67	81
582	4079	700746817H1	SOYMON013	g2078349	BLASTN	902	1e-66	81
583	4079	701007939H1	SOYMON019	g2078349	BLASTN	877	1e-64	80
584	4079	701015475H1	SOYMON019	g2078349	BLASTN	843	1e-61	82
585	4079	701097904H1	SOYMON028	g2078349	BLASTN	826	1e-60	81
586	4079	700744275H1	SOYMON013	g2078349	BLASTN	833	1e-60	80
587	4079	700907055H1	SOYMON022	g2078349	BLASTN	624	1e-59	82
588	4079	701102453H1	SOYMON028	g2078349	BLASTN	453	1e-58	80
589	4079	700795760H1	SOYMON017	g2078349	BLASTN	804	1e-58	80
590	4079	700837515H1	SOYMON020	g2078349	BLASTN	811	1e-58	84
591	4079	700943689H1	SOYMON024	g2078349	BLASTN	782	1e-56	81
592	4079	701009626H1	SOYMON019	g2078349	BLASTN	715	1e-55	85
593	4079	700978865H1	SOYMON009	g2078349	BLASTN	334	1e-51	81
594	4079	700731620H1	SOYMON010	g2078349	BLASTN	400	1e-51	79
595	4079	700891691H1	SOYMON024	g2078349	BLASTN	713	1e-50	80
596	4079	700957819H1	SOYMON022	g2078349	BLASTN	677	1e-47	79
597	4079	700563553H1	SOYMON002	g2078349	BLASTN	547	1e-46	77
598	4079	700846208H1	SOYMON021	g2078349	BLASTN	524	1e-45	79
599	4079	700965218H1	SOYMON022	g2078349	BLASTN	622	1e-43	80
600	4079	700897435H1	SOYMON027	g2078349	BLASTN	633	1e-43	80
601	-GM20444	LIB3056-010-Q1-N1-B6	LIB3056	g2078349	BLASTN	837	1e-71	74
602	12032	LIB3056-013-Q1-N1-E12	LIB3056	g2078349	BLASTN	722	1e-94	78
603	16286	LIB3029-008-Q1-B1-B11	LIB3029	g2078349	BLASTN	1047	1e-78	74
604	18700	LIB3051-043-Q1-K1-C2	LIB3051	g2078349	BLASTN	626	1e-41	75
605	3993	LIB3051-038-Q1-K1-G6	LIB3051	g2078349	BLASTN	651	1e-56	75
606	3993	LIB3051-077-Q1-K1-B8	LIB3051	g2078349	BLASTN	807	1e-56	75
607	3993	LIB3051-115-Q1-K1-B3	LIB3051	g2078349	BLASTN	511	1e-54	75
608	3993	LIB3051-054-Q1-K2-C5	LIB3051	g2078349	BLASTN	755	1e-52	75
609	3993	LIB3040-029-Q1-E1-B10	LIB3040	g2078350	BLASTX	117	1e-43	61
610	3993	LIB3040-059-Q1-E1-F9	LIB3040	g2078350	BLASTX	217	1e-42	57
611	3993	LIB3051-087-Q1-K1-A8	LIB3051	g2078349	BLASTN	368	1e-38	75
612	3993	LIB3056-001-	LIB3056	g2078349	BLASTN	520	1e-32	72

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		Q1-B1-C11						
613	3993	LIB3051-112-Q1-K1-H9	LIB3051	g2078349	BLASTN	393	1e-30	71
614	4079	LIB3056-008-Q1-N1-H10	LIB3056	g2078349	BLASTN	1357	1e-104	81
615	4079	LIB3050-022-Q1-K1-B11	LIB3050	g2078349	BLASTN	1338	1e-102	81
616	4079	LIB3051-094-Q1-K1-B8	LIB3051	g2078349	BLASTN	1088	1e-81	80
617	4079	LIB3050-021-Q1-K1-G2	LIB3050	g2078349	BLASTN	673	1e-49	77

MAIZE PUTATIVE TRANSALDOLASE

Seq No.	Cluster ID	CloneID	Library	NCBI gi	Method	Score	P-value	%Ident
618	15681	700429804H1	SATMONN01	g1323043	BLASTX	100	1e-11	37

MAIZE PHOSPHOGLUCOISOMERASE

Seq No.	Cluster ID	CloneID	Library	NCBI gi	Method	Score	P-value	%Ident
619	-700086021	700086021H1	SATMON011	g1100771	BLASTX	225	1e-28	51
620	-700169489	700169489H1	SATMON013	g1100771	BLASTX	152	1e-13	59
621	-700222638	700222638H1	SATMON011	g1100771	BLASTX	256	1e-28	60
622	-700445574	700445574H1	SATMON027	g1100771	BLASTX	143	1e-12	54
623	-700475232	700475232H1	SATMON025	g596022	BLASTN	845	1e-61	90
624	-700612774	700612774H1	SATMON033	g596022	BLASTN	1574	1e-122	95
625	14393	700222547H1	SATMON011	g1100771	BLASTX	239	1e-25	60
626	14393	700220357H1	SATMON011	g1100771	BLASTX	218	1e-23	68
627	14393	700050317H1	SATMON003	g1100771	BLASTX	120	1e-22	63
628	14393	700163544H1	SATMON013	g1100771	BLASTX	214	1e-22	62
629	15724	700207164H1	SATMON017	g1100771	BLASTX	135	1e-17	67
630	15724	700552402H1	SATMON022	g1100771	BLASTX	135	1e-11	60
631	15724	700086085H1	SATMON011	g1100771	BLASTX	137	1e-11	45
632	20643	700577051H1	SATMON031	g1100771	BLASTX	241	1e-26	66
633	20643	700201592H1	SATMON003	g1100771	BLASTX	113	1e-19	45
634	20643	700576644H1	SATMON030	g1100771	BLASTX	113	1e-17	43
635	2351	700208928H1	SATMON016	g1100771	BLASTX	274	1e-43	73
636	2351	700240758H1	SATMON010	g1100771	BLASTX	283	1e-43	79
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SOYBEAN PHOSPHOGLUCOISOMERASE

Seq No.	Cluster ID	CloneID	Library	NCBI gi	Method	Score	P-value	%Ident
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687	18663	700838363H1	SOYMON020	g1100771	BLASTX	215	1e-22	63
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689	19355	700897450H1	SOYMON027	g1100771	BLASTX	273	1e-31	74
690	19355	700744258H1	SOYMON013	g1100771	BLASTX	207	1e-29	69
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698	20088	LIB3051-014-Q1-E1-G3	LIB3051	g1100771	BLASTX	400	1e-68	73
699	31255	LIB3056-008-Q1-N1-G8	LIB3056	g1100771	BLASTX	188	1e-52	62

*Table Headings

Cluster ID

A cluster ID is arbitrarily assigned to all of those clones which belong to the same cluster at a given stringency and a particular clone will belong to only one cluster at a given stringency.

5   If a cluster contains only a single clone (a "singleton"), then the cluster ID number will be negative, with an absolute value equal to the clone ID number of its single member. The cluster ID entries in the table refer to the cluster with which the particular clone in each row is associated.

Clone ID

10   The clone ID number refers to the particular clone in the PhytoSeq database. Each clone ID entry in the table refers to the clone whose sequence is used for (1) the sequence comparison whose scores are presented and/or (2) assignment to the particular cluster which is presented. Note that a clone may be included in this table even if its sequence comparison scores fail to meet the minimum standards for similarity. In such a case, the clone is included due solely to its

15   association with a particular cluster for which sequences of one or more other member clones possess the required level of similarity.

Library

The library ID refers to the particular cDNA library from which a given clone is obtained. Each cDNA library is associated with the particular tissue(s), line(s) and developmental stage(s)

20   from which it is isolated.

NCBI gi

Each sequence in the GenBank public database is arbitrarily assigned a unique NCBI gi (National Center for Biotechnology Information GenBank Identifier) number. In this table, the

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NCBI gi number which is associated (in the same row) with a given clone refers to the particular

GenBank sequence which is used in the sequence comparison. This entry is omitted when a

clone is included solely due to its association with a particular cluster.

Method

5   The entry in the "Method" column of the table refers to the type of BLAST search that is

used for the sequence comparison. "CLUSTER" is entered when the sequence comparison

scores for a given clone fail to meet the minimum values required for significant similarity. In

such cases, the clone is listed in the table solely as a result of its association with a given cluster

for which sequences of one or more other member clones possess the required level of similarity.

10   **Score**

Each entry in the "Score" column of the table refers to the BLAST score that is generated

by sequence comparison of the designated clone with the designated GenBank sequence using

the designated BLAST method. This entry is omitted when a clone is included solely due to its

association with a particular cluster. If the program used to determine the hit is HMMSW then

15   the score refers to HMMSW score.

P-Value

The entries in the P-Value column refer to the probability that such matches occur by

chance.

%Ident

20   The entries in the "%Ident" column of the table refer to the percentage of identically

matched nucleotides (or residues) that exist along the length of that portion of the sequences

which is aligned by the BLAST comparison to generate the statistical scores presented. This

entry is omitted when a clone is included solely due to its association with a particular cluster.

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We claim:

1.   A substantially purified nucleic acid molecule that encodes a maize or soybean

phosphogluconate pathway enzyme or fragment thereof, wherein said maize or soybean

phosphogluconate pathway enzyme is selected from the group consisting of:

5   (a) glucose-6-phosphate-1-dehydrogenase or fragment thereof;

          (b) 6-phosphogluconate dehydrogenase or fragment thereof;

          (c) putative 6-phosphogluconate dehydrogenase or fragment thereof;

          (d) D-ribulose-5-phosphate-3-epimerase or fragment thereof;

          (e) ribose-5-phosphate isomerase or fragment thereof;

10   (f) putative ribose-5-phosphate isomerase or fragment thereof;

          (g) transketolase or fragment thereof;

          (h) putative transketolase or fragment thereof;

          (i) transaldolase or fragment thereof;

          (j) putative transaldolase or fragment thereof;

15   (k) phosphoglucoisomerase or fragment thereof;

2.   The substantially purified nucleic acid molecule according to claim 1, wherein said

nucleic acid molecule comprises a nucleic acid sequence selected from the group consisting of

SEQ ID NO: 1 through SEQ ID NO: 699.

3.   A substantially purified maize or soybean phosphogluconate pathway enzyme or

20   fragment thereof, wherein said maize or soybean phosphogluconate pathway enzyme is selected

from the group consisting of:

          (a) glucose-6-phosphate-1-dehydrogenase or fragment thereof;

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(b) 6-phosphogluconate dehydrogenase or fragment thereof;

(c) putative 6-phosphogluconate dehydrogenase or fragment thereof;

(d) D-ribulose-5-phosphate-3-epimerase or fragment thereof;

(e) ribose-5-phosphate isomerase or fragment thereof;

(f) putative ribose-5-phosphate isomerase or fragment thereof;

(g) transketolase or fragment thereof;

(h) putative transketolase or fragment thereof;

(i) transaldolase or fragment thereof;

(j) putative transaldolase or fragment thereof;

(k) phosphoglucoisomerase or fragment thereof;

4.   A substantially purified maize or soybean phosphogluconate pathway enzyme or

fragment thereof according to claim 3, wherein said maize or soybean phosphogluconate

pathway enzyme or fragment thereof is encoded by a nucleic acid molecule comprising a nucleic

acid sequence selected from the group consisting of SEQ ID NO: 1 through SEQ ID NO: 699.

5.   A substantially purified antibody or fragment thereof which is capable of specifically

binding to a specific maize or soybean phosphogluconate pathway enzyme or fragment thereof

according to claim 4.

6.   A transformed plant having a nucleic acid molecule which comprises:

(A) an exogenous promoter region which functions in a plant cell to cause the production

        of a mRNA molecule;

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(B) a structural nucleic acid molecule comprising a nucleic acid sequence selected from the group consisting of

(a) a nucleic acid sequence which encodes for a glucose-6-phosphate-1-dehydrogenase enzyme or fragment thereof;

(b) a nucleic acid sequence which encodes for a 6-phosphogluconate dehydrogenase enzyme or fragment thereof;

(c) a nucleic acid sequence which encodes for a putative 6-phosphogluconate dehydrogenase enzyme or fragment thereof;

(d) a nucleic acid sequence which encodes for a D-ribulose-5-phosphate-3-epimerase enzyme or fragment thereof;

(e) a nucleic acid sequence which encodes for a ribose-5-phosphate isomerase enzyme or fragment thereof;

(f) a nucleic acid sequence which encodes for an putative ribose-5-phosphate isomerase enzyme or fragment thereof;

(g) a nucleic acid sequence which encodes for a transketolase enzyme or fragment thereof;

(h) a nucleic acid sequence which encodes for a putative transketolase enzyme or fragment thereof;

(i) a nucleic acid sequence which encodes for a transaldolase enzyme or fragment thereof;

(k) a nucleic acid sequence which encodes for a putative transaldolase enzyme or fragment thereof;

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(l) a nucleic acid sequence which encodes for a phosphoglucoisomerase enzyme or fragment thereof;

(m) a nucleic acid sequence which is complementary to any of the nucleic acid sequences of (a) through (l); and

5   (C)   a 3' non-translated sequence that functions in said plant cell to cause termination of transcription and addition of polyadenylated ribonucleotides to a 3' end of said mRNA molecule.

7.   The transformed plant according to claim 6, wherein said structural gene is complementary to any of the nucleic acid sequences of (a) through (l).

10   8.   A method for determining a level or pattern in a plant cell of a phosphogluconate pathway enzyme in a plant metabolic pathway comprising:

(A)   incubating, under conditions permitting nucleic acid hybridization, a marker nucleic acid molecule, said marker nucleic acid molecule selected from the group of marker nucleic acid molecules which specifically hybridize to a nucleic acid molecule having the nucleic

15   acid sequence of SEQ ID NO: 1 through SEQ ID NO: 699 or complements thereof, with a complementary nucleic acid molecule obtained from said plant cell or plant tissue, wherein nucleic acid hybridization between said marker nucleic acid molecule and said complementary nucleic acid molecule obtained from said plant cell or plant tissue permits the detection of an mRNA for said phosphogluconate pathway enzyme;

20   (B)   permitting hybridization between said marker nucleic acid molecule and said complementary nucleic acid molecule obtained from said plant cell or plant tissue; and

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(C) detecting the level or pattern of said complementary nucleic acid, wherein the detection of said complementary nucleic acid is predictive of the level or pattern of said phosphogluconate pathway enzyme in said plant metabolic pathway.

9. The method of claim 8, wherein said level or pattern is detected by *in situ* hybridization.

5

ABSTRACT

The present invention is in the field of plant biochemistry. More specifically the invention relates to nucleic acid sequences from plant cells, in particular, nucleic acid sequences from maize and soybean associated with the phosphogluconate pathway enzymes. The invention encompasses nucleic acid molecules that encode proteins and fragments of proteins. In addition, the invention also encompasses proteins and fragments of proteins so encoded and antibodies capable of binding these proteins or fragments. The invention also relates to methods of using the nucleic acid molecules, proteins and fragments of proteins and antibodies, for example for genome mapping, gene identification and analysis, plant breeding, preparation of constructs for use in plant gene expression and transgenic plants.

248

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acgggtggtg atcatgctcg tcaaggccgg cgcgccagtt gaccagacca                410


<210>     17
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<212>     DNA
<213>     Zea mays

<400>     17

aggtggccgg acggtggtgg catcgccaat tcaactccgc atctgaatcg gcactcggca     60
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6

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gcgcgccagc tccatagtgt aggaggagga gatggcgctc acaagaatcg gtcttgctgg  120

ccttgcggtc atggggcaga accttgccct caacattgca gagaaagggt tccccatctc  180

tgtgtacaac aggacaacct ccaaggtgga cgagaccgtg cagcgtgcca aggcagaagg  240

aaaccttccc gtctacggct tccatgaccc cgcgtccttt gtgaactcca ttcagaagcc  300

acgggtggtg atcatgctcg tcaaggccgg cgcgccagtt gaccagacca tcgcgacgct  360

cgcagctcac ttggagcagg gcgactgcat catcgaatgg gggaacgag            409
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<210>        18
<211>        420
<212>        DNA
<213>        Zea mays

<400>        18
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gctccatagg aggagatggc gctcacaaga atcggtcttg ctggccttgc ggtcatgggg  120

cagaaccttg ccctcaacat tgcagagaaa gggttcccca tctctgtgta caacaggaca  180

acctccaagg tggacgagac cgtgcagcgt gccaaggcag aaggaaacct cccgtctac  240

ggcttccatg accccgcgtc ctttgtgaag tccattcaga gccacgggt ggtgatcatg  300

ctcgtcaagg ccggcgcgcc agttgaccag accatcgcga cgctcgcagc tcacttggag  360

cagggcgact gcatcatcga taggggaac gagtggtacg aggacacgga gaggagggag  420
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<210>        19
<211>        403
<212>        DNA
<213>        Zea mays

<400>        19
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gcagcgcgcc agctccatag tgtaggagga gatggcgctc acaagaatcg gtcttgctgg  120

ccttgcggtc atggggcaga accttgccct caacattgca gagaaagggt tccccatctc  180

tgtgtacaac aggacaacct ccaaggtgga cgagaccgtg cagcgtgcca aggcagaagg  240

aaaccttccc gtctacggct tccatgaccc cgcgtccttt gtgaagtcca ttcagaagcc  300

acgggtggtg atcatgctcg tcaaggccgg cgcgccagtt gaccagacca tcgcgacgct  360
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7

cgcagctcac tttgagcagg gcgactgcat catcgatggg ggg 403

<210>   20
<211>   433
<212>   DNA
<213>   Zea mays

<400>   20

ggcactttcc ctgcctgatt ggcgatttat agcggtgggg gagggaaggc cgatggtcag   60

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ggcagcgcgc cagctccata ggaggagatg gcgctcacaa gaatcggtct tgctggcctt   180

gcggtcatgg ggcagaacct tgccctcaac attgcagaga aagggttccc catctctgtg   240

tacaacagga caacctccaa ggtggacgag accgtgcagc gtgccaaggc agaaggaaac   300

cttcccgtct acggcttcca tgaccccgcg tcctttgtga agtccattca gaagccacgg   360

gtggtgatca tgctcgtcaa ggccggcgcg ccagttgacc agaccatcgc gacgctcgca   420

gctcacttgg agc   433

<210>   21
<211>   209
<212>   DNA
<213>   Zea mays

<223>   unsure at all n locations
<400>   21

gcatctgcat cggcagcgcg ncagnngnat aggaggagat ggcgctcaca agaatcggtn   60

ttgctggcct tgcggncatg gggcagaacc ttgccctnaa cattgcagag aaagggnnan   120

ccatatgtgt gnacaacagg acaacctgca aggtngacna gaccgtncag ngngncnagg   180

cagaangana ccttangntt tannnattg   209

<210>   22
<211>   271
<212>   DNA
<213>   Glycine max

<223>   unsure at all n locations
<400>   22

caagaaggaa accttcctgt ntatggctac cataacccta aattctttgt ccaatccatt   60

8

cancaagcca aggutcataa taatgcttgt caaggctgnt gcacctgttg accaaaccat   120

caagaccctc tcagcacact tnnccaaggg tgattgcatc attgatggtg caatgagtg   180

gtatgagaac actgagagaa gagagaaagc gatgtccgaa ttgggtcttc tctaccttgn   240

ggatgggagt ttcaggtggt gaagaaggtg c   271

<210>   23
<211>   240
<212>   DNA
<213>   Glycine max

<400>   23

tctcgagcga atcggctcgg aggctactta aagggcttgg aatgaagaaa ggaaataatt   60

gatcaccaat ctgcctggag gagagttgtt tgccttgcta tcaattccgg tattagcact   120

ccaggttatt tcagggatag gattttgttc ctgactgtat tgcagtcacc gaatatggag   180

caactaagga cggatatttg ggggtatatt atgggcaacg agaggttgga tgcgaattac   240

<210>   24
<211>   242
<212>   DNA
<213>   Glycine max

<223>   unsure at all n locations
<400>   24

ctgctctacc ttgggatggg agtttctggt ggtgaggaag gtgctctaat ggtccctctt   60

tgatgcctgg tggtcgttga ggcttcaaat acatagaaga tattcttctc aaggtgcagc   120

tcaagtcctg acagtggtct tgcgtactat atnnnaaggt gnctggtaat ttgtcnatga   180

tcacatggac gattgtgnat nantatgcaa ggcatattnt gagcatagca gtgcaataga   240

tc   242

<210>   25
<211>   263
<212>   DNA
<213>   Glycine max

<400>   25

cctgagttga gtttacatag ccacaacgtg gtgaagtttt atttatatta tttccaactg   60

aattgcttga tagtttgttt ccaactatg ttgtatcttt gctgatcatg ctttgtgctt   120

gatacaaaat tgtccagctc atggtgcctt tttaattttc acattttgat aagatttcct   180

tcagcgtcat ggatacatgt tatgttacac caggagttga aattttaca tttattgtta   240

acttgttgag tttaatgttg atc   263

<210>   26
<211>   253
<212>   DNA
<213>   Glycine max

<400>   26

ctctcaaata catagaagat attcttctca atgtggcagc tcaagtacct gacagtggtc   60

cttgcgtgac ttatcttggt aaaggtgggt ctggtaattt tgtgagagag attcaacaat   120

ggaatgagta atggtgaatt cagctgaatt ccaaaggctt ataaggtccg gaattcagtt   180

ggaaagtggt caattgagga ctaacaaggg gcctcctcgg attggaccaa ggaagacctc   240

cgaagttccc gga   253

<210>   27
<211>   229
<212>   DNA
<213>   Glycine max

<400>   27

cagaccttat tttttctgtc atttgcttca aatttcagga gattaattat gcgctcaacc   60

cacaacaaga ataggccttg ctggattggc tgttaatggg caaaatctgg cactcaatat   120

tgcttgaaaa gggcttccca attccggtta acaacggaac catttccaag gttattgggc   180

cataagacga agcaaaccag gaaggaaacc ttcaatttat ggggaacaa   229

<210>   28
<211>   250
<212>   DNA
<213>   Glycine max

<400>   28

aatgaatctg atcagggcaa agagcattga gaaaggttgg gacttgaagt tgggggaact   60

tgcaaggatt tggaaagggg gttgcatcat aagagcaata tttttggaca gaatcaagaa   120

10

agcatacgac agaaatccta accttgcaaa ccttcttgtg gatccagaat ttgcaaagga 180

aatagtggat agacaatctg catggagaag agttgtgtgt cttgctatca actatggcac 240

tagcacacca 250

<210> 29
<211> 87
<212> DNA
<213> Glycine max

<400> 29

ggctcgaggg ggtcttacca cactgagtgg ttcaagcttg ccaaacagtc aagaaattag 60

agtactgtag tgcagccaat caggatc 87

<210> 30
<211> 256
<212> DNA
<213> Glycine max

<400> 30

attcttctca aggtggcagc tcaagtccct gacagtggtc cttgcgtgac ttatattggt 60

aaaggtggct ctggtaattt tgtgaaaatg atccacaatg gcatcgaata tggtgacatg 120

cagctgattg cagaggccta tgatgtgctg aagtcagttg gaaagttgtc aaatgaggaa 180

ctacaaagtg tcttctcaga atggaacaag ggagaacttc tgagtttcct gattgaaatc 240

actgcagata tatttg 256

<210> 31
<211> 213
<212> DNA
<213> Glycine max

<400> 31

gcgtgactta tattggtaaa ggtggctctg gtaattttgt gacaatgatc cacaatggca 60

tcgaatctgg tgacatgcag ctgattgcag aggcctatga tgtgctgaag tcagttggaa 120

agttgtcaaa tgaggaacta caaagtgtct ctcagaatg gaacaaggga gaacttctcg 180

agtttcctga ttgacatcac tgcagatata ttt 213

<210> 32

11

<211>   268
<212>   DNA
<213>   Glycine max

<223>   unsure at all n locations
<400>   32

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ggtaattttg tgaaaatgat ccacaatggc atcgaatatg gtgacatgca gctgattgca   120

gaggcctatg atgtgctgaa gtcagttgga aagttgtcaa atgaggaact acaaagtgtc   180

tcctcagaat ggaacaaggg agaattctga gtttccgatt ganatcatgc agatatattg   240

gattcangag ataagggaga nggatacc   268

<210>   33
<211>   109
<212>   DNA
<213>   Glycine max

<400>   33

aaattttgtg aaaatgatcc acaatggaat tgagtatggt gacatgcagc tcattgctga   60

ggcctatgat gtgctaaagt cggttggaaa gttgtcaaat gaggagctg   109

<210>   34
<211>   277
<212>   DNA
<213>   Glycine max

<400>   34

gggcactggt aagtggactg ttcagcaagg tgctgaatta tcaattgctg ctcccactat   60

tgaagcatca ttggatgcaa ggttcctgag tgggttgaag gaggaaagag ttgaagctgc   120

aaaggtcttt aaatcaggtg gtattggtga tatcgtgact gatcaacctg tagacaagaa   180

aaaattggtt gatgatgtta ggaaggctct ttatgcagcc aaaatctgta gttatgcaca   240

gggaatgaat ttgatccgtg caaagagtat tgaaaag   277

<210>   35
<211>   252
<212>   DNA
<213>   Glycine max

<400>   35

12

gcaaggttcc tgagtgggtt gaaggaggaa agagttgaag ctgcaaaggt ctttaaatca   60

ggtggcattg gtgatattgt gactgatcaa cctgtagaca agcagaagtt gattgatgat   120

gttaggaagg ctctttatgc agccagaatc tgtagttatg cacagggaat gaatttgatc   180

cgtgcaaaga gtattgaaaa gggttgggat ttgaagttgg gtgaactggc ccggatttgg   240

aaagggggtt gc   252

<210>   36
<211>   262
<212>   DNA
<213>   Glycine max

<400>   36

cttgttgaca aggtcctaga caagactggc atgaagggca ctggtcaagt ggactgggca   60

gcaagctgct gaattatcaa ttgctgctcc cactattgaa gcatcattgg atgcaaggtt   120

cctgagtggg ttgaaggagg aaagacttga agctgcaaag gtctttaaat caggtggtat   180

tgctgatatc gtgactgatc aacctgtaga caagaaaaaa ttggttgatg atgttaggaa   240

ggctctttat gcagccaaaa tc   262

<210>   37
<211>   241
<212>   DNA
<213>   Glycine max

<223>   unsure at all n locations
<400>   37

tttggaatta aggatgataa gggagatgga tatcttgttg acaaggtcct agacaagact   60

ggcatgaagg gcactggtaa gtggactgtt cagcaagctg ctgaattatc aattgctgct   120

cccactattg angcatcatt ggatgcaagg ttcctgagtg ggttgaagga ggaagagttg   180

aagctgcaaa ggtctttaaa tcaggtggta ttggtgatat cgtgactgat caacctgtag   240

a   241

<210>   38
<211>   239
<212>   DNA
<213>   Glycine max

<400> 38

aaagtgtctt ctcagaatgg aacaagggag aacttctgag tttcctgatt gaaatcactg 60

cagatatatt tggaattaag gatgataagg gagatggata tcttgttgac aagcgtccta 120

gacaagactg gcatgaaggg cactggtaag tggactgttc agcaagctgc tgaattatca 180

attgctgctc ccactattga agcatcattg gatgcaaggg tcctgagtgg ggtgaagga 239

<210>   39
<211>   252
<212>   DNA
<213>   Glycine max

<400>   39

ggagatggat tcttgttgac aaggtcctag acaagactgg catgaagggc actggtaagt 60

ggactgttca gcaagctgct gaattatcaa ttgctgctcc cactattgaa gcatcattgg 120

atgcaaggtt cctgagtggg ttgaaggagg aaagagttga agctgcaaag gtctttaaat 180

caggtggtat tggtgatatc gtgactgatc aacctgtaga caagaaaaaa ttggttgata 240

tgttaggaag gc 252

<210>   40
<211>   262
<212>   DNA
<213>   Glycine max

<400>   40

ctcgagccgt tcttagacag aatcaagcag gcatatgaaa gaacccctaa tctggcaaac 60

cttcttgtgg atccagagtt tgcaaaggaa ataattgatt accaatctgc ctggaggaga 120

gttgtttgcc ttgctatcaa ttctggtatt agcactccag gtatgtctgc tagtcttgct 180

tattttgaca cttacagaag ggaaaggttg ccagctaatt tggtgcaagc tcaacgagac 240

tactttggtg ctcatacata tg 262

<210>   41
<211>   167
<212>   DNA
<213>   Glycine max

<223>   unsure at all n locations
<400>   41

14

accttcttgt ggatccagag tttgcaangg aaataatcga tcgccaatct gcctggagga   60

gagttgtttg ccttgctatc aattctggta tcagcactcc aggtatgtct gctagtctng   120

cttatnttga cacttacaga agggaaaggt nnccagctaa tttggtg   167

<210>   42
<211>   230
<212>   DNA
<213>   Glycine max

<400>   42

gtgatagcga tgtccgaatt gggtcttctc taccttggga tgggagtttc aggtggtgaa   60

gaaggtgcaa gacatggtcc ctctttgatg cctggtggtt cattcgagga ctacaagtac   120

atagaagaca ttctcctcaa ggtagacgca caagtccctg atagtggtca ttgtgtgacc   180

tacatcggca aggtggatc aggaaatttt gtgaaaatga tccacaatgg   230

<210>   43
<211>   245
<212>   DNA
<213>   Glycine max

<400>   43

gtgaaagcga tgtccgaatt gggtcttctc taccttggga tgggagtttc aggaggtgaa   60

gaaggtgcaa gacatggtcc ctctttgatg cctggtggtt cattcgaggc ctacaagtac   120

atagaagaca ttctcctcaa ggtggccgca caagtccctg atagtggtcc ttgtgtgacc   180

tacatcggca aggtggatc aggaaatttt gtgaaaatga tccacaatgg aattgagtat   240

ggtga   245

<210>   44
<211>   289
<212>   DNA
<213>   Glycine max

<400>   44

atctgcctgg aggagagttg tttgccttgc tatcaattct ggtattagca ctccaggtat   60

gtctgctagt cttgcttatt ttgacactta cagaagggaa aggttgccag ctaatttggt   120

gcaagctcaa cgagactact ttggtgctca tacatatgaa agggttgaca tagaggggtc   180

15

ttaccatact gagtggttca agcttgccaa acagtcaaga aattagatta ctgtatttga   240

gccatcagga ttttcctaat aaatgtaata ttgtctgctc agactgtat   289

<210>   45
<211>   272
<212>   DNA
<213>   Glycine max

<400>   45

tcaggtatgt ctgctagtct tgcttatttt gacacttaca gaagggaaag gttgccagct   60

aatttggtgc aagctcaacg agactacttt ggtgctcata catatgaaag ggttgacata   120

gaggggtctt accatactga gtggttcaag cttgccaaac agtcaagaaa ttagattact   180

gtatttgagc caatcaggat tttcctaata aatgtaatat tttctgctca gactgtatgc   240

tgagttgagt ttgcatatcc acaatgtggt ga   272

<210>   46
<211>   246
<212>   DNA
<213>   Glycine max

<400>   46

ctaagataca acatagttgg aaaacaaact atcaagcaat tcagttggaa ataatataaa   60

taaaacttca ccacgttgtg gctatgtaaa ctcaactcag catacagtct gagcagaaaa   120

cattacattt attaggaaaa tcctgattgg ttcaaataca gtaatctaaa ttctagactg   180

tttggcaagc ttgaaccact cagtatggta agacccctct atgtcaacca ttcatatgta   240

tgagca   246

<210>   47
<211>   156
<212>   DNA
<213>   Glycine max

<400>   47

ggggtcttac catactgagt ggttcaagct tgccaaacag tcaagaaatt agattactgt   60

atttgagcca atcaggattt tcctaataaa tgtaatattt tctgctcaga ctgtatgctg   120

agttgagttt gccaagcaat tcagttggaa ataatg   156

16

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<210>      48
<211>      250
<212>      DNA
<213>      Glycine max

<400>      48

tatggctacc atgaccccga agcttttgtt cattccattc aaaagcctag ggtgataata   60

atgcttgtta aggctggggc acctgttgac cagaccatta gaccctatc tgcatacatg   120

gaaaaaggtg actgcataat tgatggtggt aacgaatggt acgagaacac cgaaaggaga   180

gagaaatcgg tggctgaatt gggtctgctc taccttggga tgggagtttc tggtggtgag   240

gaaagtgctc                                                           250


<210>      49
<211>      170
<212>      DNA
<213>      Glycine max

<400>      49

ggcacctgtt gaccagacca ttaagaccct atctgcatac atggaaaaag gtgactgcat   60

aattgatggt ggtaacgaat ggtacgagaa caccgaaaga agagagaaat cggtggctga   120

attgggtctg ctctaccttg ggatgggagt ttctggtggt gaggaaggtg              170


<210>      50
<211>      275
<212>      DNA
<213>      Glycine max

<400>      50

gacgacagaa gggagaaatc ggtggctgaa ttgggtctgc tctacctcgg gatgggagtt   60

tctggtggtg aggaaggtgc tcgtaatggt ccctctttga tgcctggtgg ttcgtttgag   120

gctttcaaat acatagaaga tattcttctc aaggtggcag ctcaagtccc tgacagtggt   180

ccttgcgtga cttatattgg taaaggtggc tctggtaatt ttgtgaaaat gatccacaat   240

ggcatcgaat atggtgacat gcagctgatt gcaga                               275


<210>      51
<211>      256
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17

<212>   DNA
<213>   Glycine max

<400>   51

acggctgcga gaagacgaca gaaggggggaa aaaggtgact gtataattga tggtggtaac   60

gaatggtatg agaacactga aagaagagag aaagaggtgg ctgaattggg tctgctctac   120

cttgggatgg gagtttctgg tggtgaggaa ggtgctcgta atggtccctc tttgatgcct   180

ggtggttcgt ttgaggcttt caaatacata gaagatattc ttctcaaggt ggcagctcaa   240

gtacctgaca gtggtc   256

<210>   52
<211>   252
<212>   DNA
<213>   Glycine max

<400>   52

gactgccata ttgatggtgg taacgaatgg tacgagaaca ccgaaagaag agagaaatcg   60

gtggctgaat gggtctgct ctaccttggg atgggagttt ctggtggtga ggaaggtgct   120

cgtaatggtc ctctttgatg cctggtggtt cgtttgaggc tttcaaatac atagaagata   180

ttcttctcaa ggtggcagct caagtccctg acagtggtcc ttgcgtgact tatattggta   240

aaggtggctc tg   252

<210>   53
<211>   346
<212>   DNA
<213>   Glycine max

<400>   53

gtgaagttaa ggaaatcaat tatggctcaa ccctcaacaa gaatagggcc ttgctggact   60

ggctgttatg gccaaaatc tagcactcaa tattgctgag aaaggctttc ccatttctgt   120

ttataaccga accacttcca aggttgatga gactgtagaa cgagcaaaac aagaaggaaa   180

tcttccagtt tatggctacc atgaccccga agcttttgtt cattccattc aaaagcctag   240

ggtgataata atgcttgtta aggctggggc atctgttgac cagaccatta agaccctatc   300

tgcatacatg gaaaaaggtg actgcataat tgatggtggt aacgaa   346

18

<210>   54
<211>   283
<212>   DNA
<213>   Glycine max

<400>   54

ccagacctta attttctct cattcgcttc aaatttcagg aaatcaatta tggctcaacc   60

ctcaacaaga ataggccttg ctggactggc tgttatgggc caaaatctag cactcaatat   120

tgctgagaaa ggctttccca tttctgttta taaccgaacc acttccaagg ttgatgagac   180

tgtagaacga gcaaaacaag aaggaaatct tccagtttat ggctaccatg accccgaagc   240

ttttgtcatt ccattcaaaa gcctagggtg ataataatgc ttg   283

<210>   55
<211>   276
<212>   DNA
<213>   Glycine max

<400>   55

caaatttcag gaaatcaatt atggctcaac cctcaacaag aataggcctt gctggactgg   60

ctgttatggg ccaaaatcta gcactcaata ttgctgagaa aggctttccc atttctgttt   120

ataaccgaac cacttccaag gttgatgaga ctgtagaacg agcaaaacag gaaggaaatc   180

ttccagttta tggctaccat gaccccgaag cttttgttca ttccattcaa aagcctaggg   240

tgataataat gcttgttaag gctggggcac tgttg   276

<210>   56
<211>   289
<212>   DNA
<213>   Glycine max

<400>   56

cagaccttaa ttgttctctc attcgcttca aatttcagga aatcaattat ggctcaaccc   60

tcaacaagaa taggccttgc tggactggct gttatgggcc aaaatctagc actcaatatt   120

gctgagaaag ctttcccat ttctgtttat aaccgaacca cttccaaggt tgatgagact   180

gtagaacgag caaaacaaga aggaaatctt ccagtttatg ctaccatga ccccgaagct   240

tttgttcatt ccattcaaaa gcctagggtg ataataatgc ttgttaagg   289

19

<210>   57
<211>   267
<212>   DNA
<213>   Glycine max

<400>   57

cctcattcgc ttcaaatttc aggaaatcaa ttatggctca accctcaaca agaataggcc   60

ttgctggact ggctgttatg ggccaaaatc tagcactcaa tattgctgag aaaggctttc   120

ccatttctgt tttaaccgaa ccacttccaa ggttgatgag actgtagaac gagcaaaaca   180

agaaggaaat cttccagttt atggctacca tgaccccgaa gcttttgttc attccattca   240

aaagcctagg gtgataataa tgcttgt   267

<210>   58
<211>   260
<212>   DNA
<213>   Glycine max

<400>   58

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ctcaacaaga ataggccttg ctggactggc tgttatgggc caaaatctag cactcaatat   120

tgctgagaaa ggctttccca tttctgttta taaccgaacc acttccaagg ttgatgagac   180

tgtagaacga gcaaaacaag aaggaaatct tccagtttat ggctaccatg accccgaagc   240

ttttgttcat tccattcaaa   260

<210>   59
<211>   260
<212>   DNA
<213>   Glycine max

<400>   59

tgtgattcca gaccttaatt tttctctcat tcgcttcaaa tttcaggaaa tcaattatgg   60

ctcaaccctc aacaagaata ggccttgctg gactggctgt tatgggccaa aatctagcac   120

tcaatattgc tgagaaaggc tttcccattt ctgtttataa ccgaaccact tccaaggttg   180

atgagactgt agaacgagca aaacaagaag gaaatcttcc agtttatggc taccatgacc   240

ccgaagcttt tgttcattcc   260

20

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<210>      60
<211>      265
<212>      DNA
<213>      Glycine max

<400>      60

cagaccttaa tttttctctc attcgcttca aatttcaggg gatcaattat ggctcaaccc    60

tcaacaagaa tatgccttgc tggactggct gttatgggcc agaatctagc actcaatatt   120

gctgagaaag gctttcgcat ttctgtttat aaccgaacca cttccaaggt tgatgagact   180

gtagaacgag caaaacaaga aggaaatctt ccagtttatg gctaccatga ccccgaagct   240

tttgttcatt ccattcaaaa gccta                                         265


<210>      61
<211>      263
<212>      DNA
<213>      Glycine max

<223>      unsure at all n locations
<400>      61

ctagaccttta attttctct cattcgcttc aaatttcagg aaatcaatta tggctcaacc    60

ctcaacaaga ataggccttg ctggactggc tgttatgggt ccaaatctag cactcaatat   120

tgctgagaaa ggctttccca tttctgttta taaccgaacc acttccaagg ttgatgagac   180

tgtagaacta gcannacaag aaggaaatct tccagtttat ggctaccatg accccgaagc   240

ttttgttcat tccattcaaa agc                                           263


<210>      62
<211>      279
<212>      DNA
<213>      Glycine max

<400>      62

tgctctgtga ttccagacct taattttcc ctcattcgct tcaaatttca ggaaatcaat     60

tatggctcaa ccctcaacaa gaataggcct tgcacctctg ctgttatgg gccaaaatct    120

agcactcaat attgctgaga aaggctttcc catttctgtt tataaccgaa ccacttccaa    180

ggttgatgag actgtagaac gagcaaaaca agaaggaaat cttccagttt atggctacca    240

tgaccccgaa gctttttgttc attccattca aacgcctag                         279
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21

<210> 63
<211> 284
<212> DNA
<213> Glycine max

<223> unsure at all n locations
<400> 63

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caaccctcaa caagaatagg ccttgctgga ctggctgtta tgggccaaaa tctagcactc   120

natattgctg agaaaggctt tcccatttct gnttataacc gnaccacttc caaggntgat   180

gagactgtag nacgagcnaa acaggaagga aatcttccag tttatggcta ccatgacccc   240

gnagctttgt tcattccatt caaaagctag ggtgataata atgc   284

<210> 64
<211> 256
<212> DNA
<213> Glycine max

<400> 64

gtgattccag accttaattt ttctctcatt cgcttcaaat ttcaggaaat caattatggc   60

tcaaccctca acaagaatag gccttgctgg actggctgtt atgggccaaa atctagcact   120

caatattgct gagaaaggct ttcccatttc tgtttataac cgaaccactt ccaaggttga   180

tgagactgta gaacgagcaa aacaggaagg aaatcttcca gtttatggct accatgaccc   240

cgaagctttt gttcat   256

<210> 65
<211> 265
<212> DNA
<213> Glycine max

<400> 65

ccgtgctctg tgattccaga ccttaatttt tctctcattc ccttcaaatt tcaggaaatc   60

aattatggct caaccctcaa caagaatagg ccttgctgga ctggctgtta tgggccaaaa   120

tctagcactc aatattgctg agaaaggctt tcccatttct gtttataacc gaaccacttc   180

caaggttgat gagactgtag aacgagcaaa acaagaagga aatcttccag tttatggcta   240

ccatgacccc gaagcttttg ttcat   265

22

<210>   66
<211>   275
<212>   DNA
<213>   Glycine max

<223>   unsure at all n locations
<400>   66

gtgattccca gaccttattt nttctgtcat ttgcttcaaa tttcaggaga ttaattatgg   60

ctcaacccan aacaagaata ggccttnctg gattggctgt tatgggccaa aatctggcac   120

tcaatattgc tgagaaaggc ttncccattt ctgtttacaa ccgaaccact tccaaggttg   180

atgagacagt agaacgagca aaacaagaag gaaatcttcc agtttatggc taccatgacc   240

ctgaagcttt tgttcattcc attcaanagc ctagg   275

<210>   67
<211>   236
<212>   DNA
<213>   Glycine max

<400>   67

cagaccttaa tttttctctc attcgcttca aatttcagga aatcaattat ggctcaaccc   60

tcaacaagaa taggccttgc tggactggct gttatgggcc aaaatctagc actcaatatt   120

gctgagaaag ctttcccat ttctgtttat aaccgaacca cttccaaggt tgatgagact   180

gtagaacgag caaaacagga aggaaatctt ccagtttatg gctaccatga ccccga   236

<210>   68
<211>   280
<212>   DNA
<213>   Glycine max

<400>   68

cacagacctt atgatttctg tcatttacat caaatttcag gagattaatt atggctcaac   60

ccataacaag aataggcctt gctggattgg ctgttatggg ccaaaatctg gcactcaata   120

ttgctgagaa aggctttccc attctgttta caaccgaacc acttccaagg ttgatgagac   180

agtagaacga gcaaaacaag aaggaaatct tccagtttat ggctaccatg accctgaagc   240

ttttgttcat tccattcaaa agcctagggt gatactaatg   280

23

<210> 69
<211> 281
<212> DNA
<213> Glycine max

<400> 69

ctgtgattcc cagaccttat tttttctgtc atttgcttca agtctcagga gattgattat   60

ggctcaaccc acaacaagaa taggccttgc tggattggct gttatgggcc aaaatctggc   120

actcaatatt gctgagaaag ctttcccat ttctgtttac aaccgaacca cttccaaggt   180

tgatgagaca gtagaacgag caaaacaaga aggaaatctt ccagtttatg ctaccatga   240

ccctgaagct tttgttcatt ccattcaaaa gcctagggtg a   281

<210> 70
<211> 261
<212> DNA
<213> Glycine max

<400> 70

gattcccaga ccttattttt tctgtcattt gcttcaaatt tcaggagatt aattatggct   60

caacccacaa caagaatagg ccttgctgga ttggctgtta tgggccaaaa tctggcactc   120

aatattgctg agaaaggctt tcccatttct gtttacaacc gaaccacttc caaggttgat   180

gagacagtag aacgagcaaa acaagaagga aatcttccag tttatggcta ccatgaccct   240

gaagcttttg ttcattccat t   261

<210> 71
<211> 225
<212> DNA
<213> Glycine max

<400> 71

cttaatttgt ctctcattcg cttcaaattt caggaaatca attatggctc gaccctcgac   60

aagaataggc cttgctggac tggctgttat ggggcaaaat ctagcactca atattgctga   120

gaaaggcttt cccatttctg tttataaccg aaccacttcc aaggttgatg agactgtaga   180

acgagcaaaa caagaaggaa atcttccagt ttatggctac catga   225

<210> 72

<211> 265
<212> DNA
<213> Glycine max

<400> 72

ccagaccttaa atttttctct cattcgcttc agctttcagg aaatcaatta tggctcaacc   60

ctcaacaaga ataggccttg ctggactggc tgttatgggc caaaatctag cactcaatat   120

tactgagaaa ggctgtccca tttctgttta taaccgaacc acttccaagg ttgatgagac   180

tgcagaacga gcaaaacaag aaggacatct tccagtttat ggctaccatg accccgaagc   240

ttttgttcat tccattcaaa agccc   265

<210> 73
<211> 288
<212> DNA
<213> Glycine max

<223> unsure at all n locations
<400> 73

cccgcatctt ttgatccgtg ctctgtgatt cccagacctt atttntnctg tcatttgctt   60

caaatntcag gagattaatt atggctcaac ccacaacaag aataggcctt gctggattgg   120

gctgttatgg gccaaaatct ggcactcaat attgctgaga aaggctttcc catttctgtt   180

tacanccgaa ccacttccaa ggttgatgag acagtagaac gagcaaanca agaggaaat   240

cttccagttt atggctacca tgaccctgaa gcttttgttc nttccatt   288

<210> 74
<211> 259
<212> DNA
<213> Glycine max

<400> 74

gatccgtgct ctgtgattcc cagaccttat tttttctctc atttgcttca aatttcagga   60

gattaattat ggctcaaccc acaacaagaa taggccttgc tggattggct gttatgggcc   120

aaaatctggc actcaatatt gctgagaaag ctttcccat ttctgtttac aaccgaacca   180

cttccaaggt tgatgagaca gtagaacgag caaaacaaga aggaaatctt ccagtttatg   240

gctaccatga ccctgaagc   259

<210> 75
<211> 250
<212> DNA
<213> Glycine max

<400> 75

tccagacctt aatttttctc tcattcgctt caaatttcag gaaatcaatt atggctcaac   60

cctcaacaag aataggcctt gctggactgg ctgttatggg ccaatatcta gcactcaata   120

ttgctgagaa aggtttccca tttctgttta taaccgaacc acttccaagg ttgatgagac   180

tgtagaacga gcaaaacaag aaggaaatct tccagtttat ggctaccatg accccgaagc   240

ttttgttcat   250

<210> 76
<211> 220
<212> DNA
<213> Glycine max

<223> unsure at all n locations
<400> 76

cnagacctta attttttctct cattcgcttc aaatttcagg aaatcaatta tggctcaacc   60

ctcaacaaga ataggccttg ctggactggc tgttatgggc caaaatctag cactcaatat   120

tgctgagaaa ggctttccca tttcgncnta taaccgaacc acttccaagg ttgatgagac   180

tgtagaacga gcaaaacaag aaggaaatct tccagtttnt   220

<210> 77
<211> 230
<212> DNA
<213> Glycine max

<400> 77

tgtgattcca gaccttaatt tttctctcat tcgcttcaaa tgtcaggaaa tcaagtatgg   60

ctcaaccctc cacaagagta ggccttgctg gactggctgt tatgggccca aatctagcac   120

tcaatattgc tgagaaaggc tttcccattt ctgtttataa ccgaaccact tccaaggttg   180

atgagactgt agaacgagca aaacctgaag gcaatcttcc agtttatggc   230

<210> 78
<211> 259
<212> DNA

26

<213>   Glycine max

<400>   78

cttatttttt ctgtcatttg cttcaaattt caggagatta attatagctc aacccacaac   60

aagaataggc cttgctggat tggctgttat gggccaaaat ctggcactca atattgctga   120

gaaaggcttt cccatttctg tttacaaccg aaccacttcc aaggttgatg agacagtaga   180

acgagcaaaa caagaaggaa atcttccagt ttatggctac catgaccctg aagcttttgt   240

tcattccatt caaaagcct   259

<210>   79
<211>   256
<212>   DNA
<213>   Glycine max

<400>   79

cttttgatcc gtgctctgtg attcccagac cttatttttt ctgtcatttg cttcaaattt   60

caggagatta attatggctc aacccacaac aagaataggc cttgctggat tggctgttat   120

gggccaaaac tggcactcaa tattgctgag aaaggctttc ccatttctgt ttacaaccga   180

accacttcca aggttgatga cagtagaa cgagcaaaac aagaaggaaa tcttccagtt   240

tatggctacc atgacc   256

<210>   80
<211>   253
<212>   DNA
<213>   Glycine max

<400>   80

cccagacctt attttttctg tcatttgctt caaatttcag gagataatta tggctcaacc   60

cacaacaaga ataggccttg ctggattggc tgttatgggc caaaatctgg cactcaatat   120

tgctgagaaa ggctttccca tttctgttta caaccgaacc acttccaagg ttgatgagac   180

agtagaacga gcataacaag aaggaaatct tccagtttat ggctaccatg accctgaagc   240

ttttgttcat tcc   253

<210>   81
<211>   198
<212>   DNA

27

<213>   Glycine max

<400>   81

ccagacctta attttttctct cattcgcttc aaatttcagg aaatcaatta tggctcaacc   60

ctcaacaaga ataggccttg ctggactggc tgttatgggc caaaatctag cactcaatat   120

tgctgagaaa ggctttccca tttctgttta taaccgaacc acttccaagg ttgatgagac   180

tgtagaccga gcaaaaca   198

<210>   82
<211>   281
<212>   DNA
<213>   Glycine max

<400>   82

atataatata catacatata tatataactt attcccccgc atcttttgat ccgtgctctg   60

tgattcccag accttatttt ttctgtcatt tgcttcaaat ttcaggagat taattatggc   120

tcaacccaca acaagaatag gccttgctgg attggctgtt atgggccaaa atctggcact   180

caatattgct gagaaaggct ttcccatttc tgtttacaac cgaaccactt ccaaggttga   240

tgagacagta gaacgagcaa acaagaagg aaatcttcca g   281

<210>   83
<211>   245
<212>   DNA
<213>   Glycine max

<400>   83

tcgatcgggt atcacatctg aattgggact gctcctattc tgggtactat tctgagaata   60

attatggctc aacccacaac aagaataggc cttgctggat tggctgttat gggccaaaat   120

ctggcactca atattgctga gaaaggcttt cccatttctg tttacaaccg aaccacttcc   180

aaggttgatg agacagtaga acgagcaaaa caagaaggaa atcttccagt ttatggctac   240

catga   245

<210>   84
<211>   230
<212>   DNA
<213>   Glycine max

28

<400>   84

aaccgaacca cttccaaggt tgtaaacaga aatgggaaag cctttctcag caatattgag   60

tgccagattt tggcccataa cagccaatcc agcaaggcct attcttgttg tgggttgagc   120

cataattaat ctcctgaaat ttgaagcaaa tgacagaaaa aataaggtct gggaatcaca   180

gagcacggat caaaagatgc gggggaataa gttatatata tatgtatgta   230

<210>   85
<211>   88
<212>   DNA
<213>   Glycine max

<400>   85

ggctcgagct cagtcgcttc aaatttcagg aaatcaatta tggctcaacc ctcaacaaga   60

ataggccttg ctggactggc tgttatgg   88

<210>   86
<211>   202
<212>   DNA
<213>   Glycine max

<400>   86

caaaaagcaa tctagctttg catactctac ctctacttca cctcgttacc aaaactagca   60

atcatgtctg tcgagcccaa gggagatgtc ggactcattg gtctggccgt tatgggtcaa   120

aacctgatcc tcaacatgaa cgacaagggt ttcaccgtcg tcgcctacaa ccgaaccacc   180

tccaaggtcg accacttcct gg   202

<210>   87
<211>   173
<212>   DNA
<213>   Glycine max

<400>   87

caaaaagcaa tctagctttg catactctac ctctacttca cctcgttacc aaaactagca   60

atcatgtctg tcgagcccaa gggagatgtc ggactcattg gtctggccgt tatgggtcaa   120

aacctgatcc tcaacatgaa cgacaagggt ttcaccgtcg tcgcctacaa ccg   173

<210>   88

29

<211>   237
<212>   DNA
<213>   Glycine max

<400>   88

aggaaacgcc tttcctgaga agtcggaagg aagagagtga gagtgagagt gagagtgaga   60

gagatggagt ttggattttt gggtttgggg ataatgggta aggctatggc aatcaatctg   120

ctacgccatg gcttcaaggt cactatttgg aacagaaccc tctccaagtg tgatgaactc   180

gtgcaacatg gtgcttcagt tggagaaacc ccagcaactg tagtcaagaa atgcaag   237

<210>   89
<211>   255
<212>   DNA
<213>   Glycine max

<400>   89

gattggtggt acactggaaa ttaaccatgg ctcaacctgc aagcctcaca agaataggcc   60

ttgctggcct ggctgtgatg ggccaaaacc ttgctctcaa cattgctgag aaaggctttc   120

ccatttctgt ctacaaccgg accgcgtcca aggttgatga gacagttgaa agagcaaaac   180

aagaaggaaa ccttcctgtg tatggctacc atgaccctaa attctttgtc caatccattc   240

aaaagccaag ggtca   255

<210>   90
<211>   256
<212>   DNA
<213>   Glycine max

<400>   90

ctttctcgca tgaattttcg aacattgaac aggaaattaa ccatggctca acctgcaagc   60

ctcacaagaa taggccttgc tggcctggct gtgatgggcc aaaaccttgc tctcaacatt   120

gctgagaaag ctttcccat ttctgtctac aaccggaccg cgtccaaggt tgatgagaca   180

gttgaaagag caaaacaaga aggaaacctt cctgtgtatg ctaccatga ccctaaattc   240

tttgtccaat ccattc   256

<210>   91
<211>   256
<212>   DNA

30

<210> 213   Glycine max

<400>   91

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cacccagatc tcaattttct gcaatttcac tcagaccagg aaattaacca tggctcaacc    60

tgcaagcctc acaagaatag gccttgctgg cctggctgtg atgggccaaa accttgctct   120

caacattgct gagaaaggct ttcccatttc tgtctacaac cggaccgcgt ccaaggttga   180

tgagacagtt gaaagagcaa acaagaagg aaaccttcct gtgtatggct accataaccc   240

taaattcttt gtccaa                                                   256
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<210>   92
<211>   249
<212>   DNA
<213>   Glycine max

<400>   92

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cgatgccaca acttctgtgt tggattggtg gtacactgga aattaaccat ggctcaaaca    60

acaagcctca caagaatagg ccttgctggc ctggctgtga tgggccaaaa ccttgctctc   120

aacattgctg agaaaggctt tcccatttct gtctacaacc ggaccgcgtc caaggttgat   180

gagacagttg aaagagcaaa acaagaagga aaccttcctg tgtatggcta ccatgaccct   240

aaattcttt                                                           249
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<210>   93
<211>   250
<212>   DNA
<213>   Glycine max

<400>   93

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ccagatctca attttctgca atttcactca gaccaggacc ttaaccatgg ctcaacctgc    60

aagcctcaca agaataggcc ttgctggcct ggctgtgatg gccaaaacc ttgctctcaa   120

cattgctgac aaaggctttc ccatttctgt ctacaaccgg accgcgtcca aggttgatga   180

gacagttgaa agagcaaaac aagaaggaaa ccttcctgtg tatggctacc ataacctcaa   240

attctttgtc                                                          250
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<210>   94
<211>   273
<212>   DNA
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31

<213>    Glycine max

<400>    94

gttaatttgc accttttgtt tctctctaga aattagaagt tcatgcttaa actttacctt    60

gatacttctt tctcgcatga attttcgaac attgaacagg aaattaacca tggctcaacc    120

tgcaagcctc acaagaatag gccttgctgg cctggctgtg atgggccaaa accttgctct    180

caacattgct gagaaaggct ttcccatttc tgtctacaac cggaccgcgt ccaaggttga    240

tgagacagtt gaaagagcaa aacaagaagg aaa    273


<210>    95
<211>    250
<212>    DNA
<213>    Glycine max

<400>    95

gttaatttgc accttttgtt tctctctaga aattagaagt tcatgcttaa actttacctt    60

gatacttctt tctcgcatga attttcgaac attgaacagg aaattaacca tggctcaacc    120

tgcaagcctc acaagaatag gccttgctgg cctggctgtg atgggccaaa accttgctct    180

caacattgct gagaaaggct ttcccatttc tgtctacaac cggaccgcgt ccaaggttga    240

tgagacagtt    250


<210>    96
<211>    307
<212>    DNA
<213>    Glycine max

<400>    96

caacagtgca tgcttgcaat tcaacttagt ctacagtgtc cttgtatatt actcttttgt    60

ccttgctcac ttgatgcttt ctacaatctc tgggacaccc agatctcaat tttctgcaat    120

ttcactcaga ccaggaaatt aaccatggct caacctgcaa gcctcacaag aataggcctg    180

ctggcctggg ctgtgatggg ccaaaacctt gctctcaaca ttgctgagaa aggctttccc    240

atttcgtcta caaccggacc gcgtccaagg ttgatgagac agttgaaaga gcaaacaaga    300

aggaact    307


<210>    97

32

<211>    241
<212>    DNA
<213>    Glycine max

<400>    97

ctaaaaagca cttcttagtt ctccctctcc cactaaaaac catagtactc tagataataa    60

ttaacatcaa ccctcactcc ttcgcacacc aaacccttcc ttcctatctc tcactaatct    120

aatggaatcc gcagcactgt cgcgcatagg cctggcgggc ctggcggtga tgggccaaaa    180

cctagcccta gacatcgcag aaaagggggtt cccgatctcc gtgtacaacc gcacggcctc    240

t                                                                    241


<210>    98
<211>    401
<212>    DNA
<213>    Glycine max

<400>    98

gcgtccatac gactgcgaga agacgacaga aggggatgtt aagaaggctc tttatgcagc    60

caaaatctgt agttatgcac agggaatgaa tttgatccgt gcaaacagta ttgagcgggg    120

ttgggatttg aagttgggtg aactggcccg gatttggaaa gggggttgca ttattagagc    180

aatattctta gacagaatca agcaggcata tgaaagaaac cctaatctgg caaaccttct    240

tgtggatcca gagtttgcac aggaaatcat tgattaccaa tctgcctgca ggagagttgt    300

ttgccttgct atcaattctg gtattagcac tccaggtatg tctgctaatc ttgcttattt    360

tgacacttac agaaaggaac agtttccagc caatttggtg c                        401


<210>    99
<211>    435
<212>    DNA
<213>    Glycine max

<400>    99

cccacgcgtc cgtacggctg cgagaagacg acagaaggga gaaaaaattg gttgatgatg    60

ttaggaaggc tctttatgca gccaaaatct gtagttatgc acagggaatg aatttgatcc    120

gtgcaaagag tattgaaaag ggttgggatt tgaagttggg tgaactggcc cggatttgga    180

aaggtggttg catcattaga gcaatattct tagacagaat caagcaagcg tatgatagaa    240


33

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accctaatct ggcaaacctt cttgtggatc cagagtttgc aaaggaaata atcgatcgcc    300

aatctgcctg gaggagagtt gtttgccttg ctatcaattc tggtatcagc actccaggta    360

tgtctgctag tcttgcttat tttgacactt acagaaggga aaggttgcca gctaatttgg    420

tgcaagctca acgag                                                     435


<210>      100
<211>      376
<212>      DNA
<213>      Glycine max

<400>      100

cacgcgtcca tacggctgcg agaagacgac agaagggat gttaggaagg ctctttatgc     60

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gggttgggat ttgaagttgg gtgaactggc ccggatttgg aaagggggtt gcattattag    180

agcaatattc ttagacagaa tcaagcaggc atatgaaaga aaccctaatc tggcaaacct    240

tcttgtggat ccagagtttg caaaggaaat aattgattac caatctgcct ggaggagagt    300

tgtttgcctt gctatcaatt ctggtattag cactccaggt atgtctgcta gtcttgctta    360

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<223>      unsure at all n locations
<400>      101

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ctcaaccctc aacaagaata ggccttgctg gactggctgt tatgggccaa aatctagcac    180

tcaatattgc tgagaaaggc tttcccattt ctgtttataa ccgaaccact tccaaggttg    240

atgagactgt agaacgagca aaacaagaag gaaatcttcc agtttatggc taccatgacc    300

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<210>      102
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34

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gactactttg gtgctcatac atatgaaagg gttgacatag aggggtctta ccatactgag   120

tggttcaagc ttgccaaaca gtctagaatt tagattactg tatttgaacc aatcaggatt   180

ttcctaataa atgtaatgtt ttctgctcag actgtatgct gagttgagtt tacatagcca   240

caacgtggtg aagttttatg tatattattt ccaactgaat tgcatgatag tttgttttcc   300

aactatgttg tatctttgct gattatgctt tgtgcttgat acaaaattgt ccca         354


<210>      103
<211>      399
<212>      DNA
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<223>      unsure at all n locations
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catttgcttc aaatttcagg gagattaatt atggctcaac ccacaacaag aataggcctt   120

gctggattgg ctgttatggg ccaaaatctg gcactcaata ttgctgagaa aggctttccc   180

atttctgttt acaaccgaac cacttccaag gttgatgaga cagtagaacg agcaaaacaa   240

gaaggaaatc ttccagttta tggctaccat gaccctgaag cttttgttca ttccattcaa   300

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aacctatctg cgtacatgga anaaagtgac tgtataatt                         399


<210>      104
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<400>      104

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ctgaaggacg agcgggtgga tgcctccaag atcttccatg gtgactacta ctccaccggc   120

tcgccggtgg acaaggcgca ctggttggag gacgtgatgc aggccctgta cgcgtccaa    179
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35

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<400>   105

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aattaagaga atcaaactgt gcgtacctac atcacagtaa aactgaagct acacaatgtt   120

cttcacttgc caaccataca gtacagcatt atttgaagta ctcgacttgg atctagaagc   180

ataaagataa caatagtaaa acaaaagata acccacagag agacatcaca caaagcagac   240

aacatcactt ctcataccaa ccaattcctc   270

<210>   106
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<212>   DNA
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<223>   unsure at all n locations
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acattgttct caaggtggct gctcaggtcc ctgacagtgg cccgtgtgtn acgtacattg   120

gcaaaggtgg atcgggcaac tttgtcaaga tggttcacaa cggaatcgag tatgggcgat   180

atgcagctga tttccgaggc ttacgacgtt ctcaagtcgg tcggtaagct caccaacagt   240

gagctgcacc aggtgttctc cgagtggaac aagggcgagt cctgagttct t   291

<210>   107
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<212>   DNA
<213>   Zea mays

<223>   unsure at all n locations
<400>   107

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tcaagatggt gcacaacggg ancgagtacg gcgacatgca gcaccatcgc cgaggcgtac   120

gacgtgctcc gcaggctcgg gggcctgtcc aactccgaga tcgccgatgt cttcgctgag   180

tggaacaggg gggagctcga gagcttcctg gtcnagatca ccgccgacat tttcaccgtg   240

gctgacccgt tggacgggag cgggagtggc ggcggggcgt ggttgat   287

<210>   108
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<212>   DNA
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caactccgag atcgccgacg tcttcgcgga gtggaacagg ggggagctcg agagcttcct 120

ggtccagatc atcgccgaca ttttcatcgt gctgacccgt tagactggag ctggatcggc 180

ggtcaggacg ct   192

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cgaggcttat gatttactca gtcggtgag taagctcatc aacagcgagc tgcatcaggt 180

attctctgag tgtgaatcaa ggtgagctcc tcagtatctt gattaagatc acggccgaca 240

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<210>   110
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<212>   DNA
<213>   Zea mays

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cgagaccgtg ccacgtgcca acgcagtacg aaaccttccc gtctagggct tccatgaccc 180

cgcgttcgtt gtgaagtcca ttcagaagcc acgggtggtg atcatgctcg tcaaagccgg 240

cgcgcagttg accagaccat cgcgactctc gcagctcact tggagcaggg cgactgcatc 300

37

atcgctcgtg ggaacgagtg gtacg   325

<210>   111
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<212>   DNA
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<400>   111

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atcgaagcgt tcttggactc gaggttcctg agcgggctga aggacgagcg ggtggaggcc   120

tccaagatct tccagggtga ctactactcc accggctcgc cggtggacaa ggcgcagctg   180

gtggaggacg tgaggcaggc cctgtacgcg tacaagatct gc   222

<210>   112
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<213>   Zea mays

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ctcagagaaa ggatggggcc tcaaccttgg tgagctagcg aggatctgga agggagggtg   180

catcatccgt gccatcttcc tcgaccgcat caagaaggcg tacgatagga accctaacct   240

tgccaacctc ctcgttgacc ccgagttcgc ccaggagatc atagacaggc aagctgcctg   300

gcgcagggtt gtctgccttg ccatcaacaa tggc   334

<210>   113
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ggcatgaaca tcatcaaggc caagagcgcg gagaaaggct ggggcgtcga cctcggcgaa   180

ctggcacagg atctagaagg gcgggtgcat catccgcgcc atcttcctgg accgcatcaa   240

38

gaaggcctac gacaggaacc cgggcctcgc cagcctgctc gtagaccccg agttcgcgca   300

ggagatcatg gaca   314

<210>   114
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gggagggtgc atcatccgtg ccatcttcct cgaccgcatc aagaaggcgt acgataggaa   180

ccctaacctt gccaacctcc tcgttgaccc cgagttcgcc caggagatca tagacaggca   240

agctgcctgg cgcagggttg tctgccttgc c   271

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<212>   DNA
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tgcctccaag atctgcagtt acgcgcaggg catgaacatc atcaaggcca agagctcaga   120

gaaaggatgg ggcctcaacc ttggtgagct agcgaggatc tggaagggag ggtgcatcat   180

ccgtgccatc ttcctcgacc gcatcaagaa ggcgtacgat aggaacccta accttgccaa   240

cctcctcgtt gaccccgagt tcgcccagga g   271

<210>   116
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<212>   DNA
<213>   Zea mays

<400>   116

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atcatcaagg ccaagagctc agagaaagga tggggcctca accttggtga gctagcgagg   120

atctggaagg gagggtgcat catccgtgcc atcttcctcg accgcatcaa gaaggcgtac   180

39

gataggaacc ctaaccttgc caacctcctc gttgaccccg agttcgccca ggagatcata   240

gacaggcaag ctgcctggcg cagggttgtc tgccttgcca tcaacaatg   289

<210>   117
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<212>   DNA
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<400>   117

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cctcggcgag ctggccagga tctggaaggg cgggtgcatc atccgcgcca tcttcctgga   120

ccgcatcaag aaggcctacg acaggaaccc gggcctcgcc agcctgctcg tagaccccga   180

gttcgcgcag gagatcatgg acaggcaggc ggcgtggcgc agggtggtgt gcctcgccat   240

caacaacggc gtcagacccc gggaat   266

<210>   118
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gcgaggcccg ggttcctgtc gtaggccttc ttgatgcggt ccaggaagat ggcgcggatg   120

atgcacccgc ccttccagat cctggccagc tcgccgaggt tgagcccca gcctttctcc   180

gcgctcttgg ccttgatgat gttcatgccc tgcgcgtagt gcagatcttg gacgcgtaca   240

gggcctgcct cacgtcctcc acca   264

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<212>   DNA
<213>   Zea mays

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gttacgcgca aggcatgaac agcatcaagg ccaagagctc agagaaagga tggggcctca   120

accttggtga gctagcgagg atctggaagg gagggtgcat catccgtgcc atcttcctcg   180

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accgcatcaa gaaggcgtac dataggaacc ctaaccttgc caacctcctc gttgaccccg   240

agttcgccca ggag                                                      254


<210>      120
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agatcttcca gggtgactac tactccaccg gctcgccggt ggacaaggcg cactggtgga   120

ggacgtgagg caggccctgt acgcgtccaa gatctgcagc tacgcgcagg gcatgaacat   180

catcaaggcc aagagcgcgg agaaaggctg ggggctcaac ctcggcgagc tggccaggat   240

ct                                                                   242


<210>      121
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<212>      DNA
<213>      Zea mays

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tccgcgccat cttcctggac cgcatcaaga aggcctacga caggaacccg ggcctcgcca   180

gcctgctcgt agaccccgag ttcgcgcagg agatcatgga caggc                   225


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<212>      DNA
<213>      Zea mays

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agaaaggctg ggggctcaac ctcggcgagc tggccaggat ctggaagggc gggtgcatca   120

tccgcgccat cttcctggac cgcatcaaga aggcctacga caggaacccg ggcctcgcca   180

gcctgctcgt agaccccgag ttcgcgcagg agatcatgga                         220
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41

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ctggcgcagg gttgtctgcc ttgccatcaa caatggcgtt agcaccccag gcatgtctgc   180

aagtctggcc tacttcgact cgtaccgaag agttaggttt cgcgaaactg tggtggaggc   240

tcagagag   248

<210> 124
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<212> DNA
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agaaaggctg ggggctcaac ctcggcgagc tggccaggat ctggaagggc gggtgcatca   120

tccgcgccat cttcctggac cgcatcaaga aggcctacga caggaacccg ggcctcgcca   180

gcctgctcgt agaccccgag ttcgcgcag   209

<210> 125
<211> 210
<212> DNA
<213> Zea mays

<400> 125

acgcgtccaa gatctgcagc tacgcgcagg gcatgaacat catcaaggcc aagagcgcgg   60

agaaaggctg ggggctcaac ctcggcgagc tggccaggat ctggaagggc gggtgcatca   120

tccgcgccat cttcctggac cgcatcaaga aggcctacga caggaacccg ggcctcgcca   180

gcctgctcgt agaccccgag ttcgcgcagg   210

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<212> DNA

<213>　　　Zea mays

<400>　　　126

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agaaaggctg ggggctcaac ctcggcgagc tggccaggat ctggaagggc gggtgcatca　120

tccgcgccat cttcctggac cgcatcaaga aggcctacga caggaacccg ggcctcgcca　180

gcctgctcgt agaccccgag ttcgcg　　206

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tgctcgtaga ccccgagttc gcgcaggaga tcatggacag gcaggcagcg tggcgcaggg　120

tggtgtgcct cgccatcaac aacggcgtca caccccggga atgtccgcta gcctgg　176

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<213>　　　Zea mays

<400>　　　128

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caaggccaag agcgcggaga aaggctgggg gctcaacctc ggcgagctgg ccaggatctg　120

gaagggcggg tgcatcatcc gcgcca　146

<210>　　　129
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<212>　　　DNA
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tgaacatcat caaggccaag agcgcggaga aaggcttggg gctcggcctc ggcgagctgg　120

ccaggatctg gaagggcggg tgcatcatcc gcgccatctt cctggaccgc atcaagaatg　180

cctacga   187

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acc   123

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<212>   DNA
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ccttgccaac ctcctcgttg acg   83

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ggacttgcgg tggcagcgcc acgattgccg cgtcgctgga cgggaggtac ctctcagggt   120

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gttggagacg gttaatgtcg acaagaaggt gctggtggat acggtcaggc aagcgctcta   240

cgcctccaag atttgcagct atgcgcaggg   270

<210>   133
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44

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ccgcgtcgca ggacgggagg tacctctcag ggttgaagga cgaacgggtc gcagccgctg   120

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agggaatgaa tctgctgc   258

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tctttgtaag ttaattattt atatgaa   87

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cggtggacaa ggcacagctg atcgaggacg tgaggcaagc tctatatgcc tccaagatct   240

gcagttacgc gcagggcatg aacatcatca aggccaagag ctcagagaaa ggatggggcc   300

tcaaccttgg tg   312

45

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<212>   DNA
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aggtgttctc tgagtggaac aagggtgagc tcctcagttt cttgattgag atcacggccg   180

acatctttgg tatcaaggat gacaagggtg aaggctacct ggtcgacaag gtcctggaca   240

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ctgctcc   307

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<212>   DNA
<213>   Zea mays

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tcganatcac ggccgacatc tttggcatca aggacgagca tggcgatggc tacctagtgg   180

acaaggtcct tgacaagacc gggatgaaag ggacagggaa gtggacggtg cagcaggccg   240

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ggctg   305

<210>   139
<211>   356
<212>   DNA
<213>   Zea mays

<223>   unsure at all n locations
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gaacaagggt gagctcctca gtttcttgat tgagatcacg gccgacatct ttggtatcaa   120

46

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ggatgacaag ggtgaaggct acctggtcga caaggtcctg gacaagaccg ggatgaaggg    180

aactgggaaa tggacagtcc agcaggctgc tgagctttct gtagctgctc ctacaatcga    240

ggcgtccttg gactccaggt tcctcagcgg tctaaggacg agcgcgttga ggcttccana    300

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<223>        unsure at all n locations
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tggtatcaag gatgacaagg gtgaaggcta cctggtcgac aaggtcctgg acaagaccgg    120

gatgaaggga actgggnaat ggacagtcca gcaagctgct gaacttcctg tagctgctcc    180

tacaatcaag gcgtccttgg actccaggtc cctcagcggt ctgaatgacg accgcgttga    240

ggcttccaaa atcttccaag gtgactactc cactggccta ccggtggaca aggcacagct    300

gatggaggac gt                                                        312


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<212>        DNA
<213>        Zea mays

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atcaggtgtt ctctgagtgg aacaagggtg agctcctcag tttcttgatt gagatcacgg    180

ccgacatctt tggtatcaag gatgacaagg gtgaaggcta cctggtcgac aaggtcctgg    240

acaagaccgg gatgaaggga actgggaaat ggaca                               275


<210>        142
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<213>        Zea mays

<400>        142
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47

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tctttggcat caaggacgag catggcgatg gctacctggt ggataaggtc cttgacaaga     120

ccgggatgaa agggacaggg aagtggacgg tgcagcaggc cgccgagctg tcggtggccg     180

ctcctacgat cgaggcgtcc ttggactcga ggttcctgag cgggctgaag gacgagcggg     240

tggaggcctc caagatcttc cagggtga                                       268


<210>      143
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<212>      DNA
<213>      Zea mays

<400>      143

cgacgttctc aagtcggtcg gtaagctcac caacagtgag ctgcaccagg tgttctccga      60

gtggaacaag ggcgagctcc tgagcttctt gatcgagatc acggccgaca tctttggcat     120

caaggacgag catggcgatg gctacctggt ggacaaggtc cttgacaaga ccgggatgaa     180

agggacaggg aagtggacgg tgcagcaggc cgccgagctg tcggtggccg ctcctacgat     240

cgaggcgtcc ttggactcga ggttcctga                                      269


<210>      144
<211>      267
<212>      DNA
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<400>      144

ggcaaaggtg gatcgggcaa ctttgtcaag atggttcaca acggaatcga gtatggcgat      60

atgcagctga tttccgaggc ttacgacgtt ctcaagtcgg tcggtaagct caccaacagt     120

gagctgcacc aggtgttctc cgagtggaac aagggcgagc tcctgagctt cttgatcgag     180

atcacggccg acatctttgg catcaaggac gagcatggcg atggctacct agtggacaag     240

gtccttgaca agaccgggat gaaaggg                                        267


<210>      145
<211>      247
<212>      DNA
<213>      Zea mays

<400>      145
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48

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aaggtcctgg acaagaccgg gatgaaggga actgggaaat ggacagtcca gcaggctgct   120

gagctttctg tagctgctcc tacaatcgag gcgtccttgg actccaggtt cctcagcggt   180

ctgaaggacg agcgcgttga ggcttccaaa atcttccaag gtgactactc cactggccta   240

ccggtgg                                                             247
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<210>   146
<211>   265
<212>   DNA
<213>   Zea mays

<223>   unsure at all n locations
<400>   146

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cgtacnnttn gcanangtgg atcgggcaac tttgtcaaga tggtncacaa cggaatcgag    60

tatggcgata tgcagctgat ttccgangct tacgacgttc tcaagtcggt cggtaagctc   120

accaacagtg agnngcacca ngtgttctcc gantggaaca anggnnagct cctgngcttc   180

ttgatcgnga tnncggccga natcnttggc atcaaggacg agcatggcga tggctaccta   240

ntggncaagg tccntgacaa gaccg                                         265
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<210>   147
<211>   216
<212>   DNA
<213>   Zea mays

<400>   147

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gtccagcagg ctgctgagct ttctgtagct gctcctacaa tccaggcgtc cttggactcc    60

aggttcctca gcggtctgaa ggactagcgc gttgaggctt ccagaatctt ccaaggtgac   120

tactccactg gcctaccggt ggacaatgca cagctgatcg aggacgtgag gcaagctcta   180

tatgcctcca ggatctgcag ttacgcgcag ggcatg                             216
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<210>   148
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<213>   Zea mays

<400>   148
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caagggtgag ctcctcagtt tcttgattga gatcacggcc gacatctttg gtatcaagga   60

tgacaagggt gaaggctacc tggtcgacaa ggtcctggac aagaccggga tgaagggaac  120

tgggaaatgg acagtccagc aggctgctga gctttctgta gctgctccta caatcgaggc  180

gtccttggac tccaggttcc tcaccgtctt aaaggacgac cgcgttgagg cttccaaaat  240

cttccaaggt ggatat                                                  256


<210>      149
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<212>      DNA
<213>      Zea mays

<400>      149

aaacagcgag ctgcatcagg tgttctctga gtggaacaag ggtgagctcc tcagtttctt   60

gattgagatc acggccgaca tctttggtat caaggatgac aagggtgaag ctacctggt  120

cgacaaggtc ctggacaagc cgggatgaag ggaactggga aatggacact ccaaca     176


<210>      150
<211>      185
<212>      DNA
<213>      Zea mays

<400>      150

cgacgttctc aagtcggtcg gtaagctcac caacagtgag ctgcaccagg tgttctccga   60

gtggaacaag ggcgagctcc tgagcttctt gatcgagatc acggccgaca tctttggcat  120

caaggacgag catggcgatg ctacctggt ggacaaggtc cttgacaaga ccgggatgaa  180

aggga                                                              185


<210>      151
<211>      136
<212>      DNA
<213>      Zea mays

<400>      151

caaacagcga gctgcatcag gtgttctctg agtggaacaa ggggcggctc ctcagtttct   60

tgattgagat cacggccgac atctttggta tcaaggatga caagggtgaa ggctacctgg  120

tcgacaaggt cctgga                                                  136
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50

<210> 152
<211> 282
<212> DNA
<213> Zea mays

<400> 152

cggcgctcac acgtacgaga gggacaggct tcccgccaac ctggtgcagg ctcagagaga   60

ctacttcggc gctcacacgt acgagagggt tgacatgcct ggttctttcc acaccgagtg   120

gttcaagatt gcgcgcaact ccaagatctg aacatggcct cgtgtttgca tatgccagta   180

tgccaccgtg tcgagtaatc actcatatta ctgcttgcag ggaggaactg tgtttgattt   240

ttatttccca tgcgcaatgc ttaatttagg tcaggaagtc ca   282

<210> 153
<211> 248
<212> DNA
<213> Zea mays

<400> 153

gcacgagcag ggataggctt cccgccaacc tggtgcaggc tcagagagac tacttcggcg   60

ctcacacgta cgagagggtt gacatgcctg gttctttcca caccgagtgg ttcaagattg   120

cgcgcaactc caagatctga acatggcctc gtgtttgcat atgccagtat gccaccgtgt   180

cgagtaatca atcatattac tgcttgcagg gaggaactgt gtttgatttt tattttccat   240

gcgcaatg   248

<210> 154
<211> 254
<212> DNA
<213> Zea mays

<400> 154

gcgcgcaact ccaagatctg aacatggcct cgtgtttgca tatgccagta tgccaccgtg   60

tcgagtaatc aatcatatta ctgcttgcag ggaggaactg tgtttgattt ttattttcca   120

tgcgcaatgc ttaatttagg tcaggaagtc caaagtctct cccattgttt tcctgtaaga   180

gctaagcagt accagatgga gaaccttata tttgctggaa catgaataga agcatttgac   240

atgcttgtgc ttac   254

51

<210> 155
<211> 236
<212> DNA
<213> Zea mays

<400> 155

gcacgagatt gcgcgcaact ccaagatctg aacatggcct cgtgtttgca tatgccagta   60

tgccaccgtg tcgagtaatc aatcatatta ctgcttgcag ggaggaactg tgtttgattt   120

ttattttcca tgcgcaatgc ttaatttagg tcaggaagtc caaagtctct cccattgttt   180

tcctgtaaga gctaagcagt accagatgga gaaccttata tttgctggaa catgaa   236

<210> 156
<211> 197
<212> DNA
<213> Zea mays

<400> 156

agacaggcaa gctgcctggc gcagggttgt ctgccttgcc atcaacaatg gcgttagcac   60

cccaggcatg tctgcaagtc tggcctactt cgactcgtac cgcagggaca ggcttcccgc   120

caacctggtg caggctcaga gagactactt cggcgctccc acgtacgaga gggttgacat   180

gcctggttct ttccaca   197

<210> 157
<211> 281
<212> DNA
<213> Zea mays

<400> 157

cggacgcgtg ggcggacgcg tgggcggacg cgtgggggca agctgcctgg cgcagggttg   60

tctgccttgc cactcaacaa tggcagttac accccaggca tgtctgcaca gtctggccta   120

cttcgactcg taccgcagga caggcttccc gccaacctgg tgcaggctca gagagactac   180

ttcggcgctc acacgtacga gagggttgac atgcctggtt ctttccacac cgagtggttc   240

aagattgcgc gcaactccaa gatctgaaca tggcctcgtg t   281

<210> 158
<211> 249
<212> DNA

52

<213>   Zea mays

<400>   158

cttgccatca acaatggcgt tacaccccag gcatgtctgc aagtctggcc tacttcgact   60

cgtaccgcag gacaggcttc ccgccaacct ggtgcaggct cagagagact acttcggcgc   120

tcacacgtac gagagggttg acatgcctgg ttctttccac accgagtggt tcaagattgc   180

gcgcaactcc aagatctgaa catggcctcg tgtttgcata tgccagtatg ccaccgtgtc   240

gagtaatca   249

<210>   159
<211>   150
<212>   DNA
<213>   Zea mays

<400>   159

gggaggaact gtgtttgatt tttattttcc atgcgcaatg cttaatttag gtcaggaagt   60

ccaaagtctc tcccattgtt ttcctgtaag agctaagcag taccagatgg agaaccttat   120

atttgctgga acatgaataa aagcatttga   150

<210>   160
<211>   133
<212>   DNA
<213>   Zea mays

<400>   160

gtaagtctgg cctacttcga ctcgtaccgc agggacaggc ttcccgccaa cctggtgcag   60

gctcagagag actacttcgg cgctcacacg tacgagaggg ttgacatgcc tggttctttc   120

cacaccgaat ggt   133

<210>   161
<211>   72
<212>   DNA
<213>   Zea mays

<400>   161

attgcgcgca actccaagat ctgaacatgg cctcgtgttt gcatatgcca gtatgccacc   60

gtgtcgagta at   72

53

<210>   162
<211>   327
<212>   DNA
<213>   Zea mays

<223>   unsure at all n locations
<400>   162

atcaggggga ctgtatcgtc gatggtggca acgagtggta cgagaacacg gagaggaggg   60

agaaggcgat ggaggagcgc gggctcctat atcttggcat gggcgtctcc ggaggagagg   120

agggtgcccg caatggcccg tccttgatgc ccggggggctc cttcgaggca tacaagtaca   180

ttgaagatat tcttctcaag gtggctgctc aggtacctga cagcggcccg tgcgtcacat   240

atattggcaa aagtggatca ggcaacttcg tcaagatggt tcacaatgga attgaatatg   300

gtgacatgcn acttatcgcc gaggctt   327

<210>   163
<211>   331
<212>   DNA
<213>   Zea mays

<223>   unsure at all n locations
<400>   163

cgagtggtac gagaacacgg agaggangga gaaggcgatg gaggagcgcg ggctcctata   60

tcttggcatg ggcgtctccg gaggagagga nggtgcccgc aatggcccgt ccttgatgcc   120

cggggggctcc ttcgaggcat acaagtacat tgaagatatt cttctcaagg tggctgctca   180

ggtacctgac agcggcccgt gcgtcacata tattggcaaa ggtggatcag gcaactttgt   240

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tgttctcaag tcggtgggta actaacaaac a   331

<210>   164
<211>   297
<212>   DNA
<213>   Zea mays

<223>   unsure at all n locations
<400>   164

cacggagagg agggagaagg ccatggagga gcgcggcctc ctgtatcttg gcatgggtgt   60

ctctggagga gagganggtg cccgcaacgg cccgtccttg atgcccggag gctcgttcga   120

54

ggcttacaag tacgtcgaag acattgtcct caaggtggct gctcaggtcc ctgacagtgg   180

cccgtgtgtc acgtacattg gcaaaggtgg atcgggcaac tttgtcaaga tggttcacaa   240

cggaatcgag tatggcgata tgcagctgat ttccgaggca tacgacgttc tcaagtc   297

<210>   165
<211>   324
<212>   DNA
<213>   Zea mays

<400>   165

ggtggccgga cggtggtggc atcgccaatt caactccgca tctgaatcgg cactcggcag   60

cgcgccagtc catagtgtag gaggaggaga tggcgctcac aagaatcggt cttgctggcc   120

ttgcggtcat ggggcagaac ccttgcctca agcattgcag agaaagggtt ccccatctct   180

gtgtacaaca ggacaacctc caaggtggac gagaccgtgc agcgtgccaa ggcagaagga   240

aaccttcccg tctacggctt ccatgacccc gcgtcctttg tgaactccat tcagaagcca   300

cgggtggtga tcatgctcgt caag   324

<210>   166
<211>   287
<212>   DNA
<213>   Zea mays

<400>   166

gccacgggtg gtgatcatgc tcgtcaaggc cggcgacaca gttgtgcaga ccatcgcgac   60

gctcgcagct cacttggagc agggcgactg cgtcatcgat gggggggaacg agtggtacga   120

gaacacggag aggaggggaga aggccatgga ggagcgcggc ctcctgtatc ttggcatggg   180

tgtctctgga ggagaggagg gtgcccgcaa cggcccgtcc ttgatgcccg gaggctcgtt   240

cgaggcttac aagtacgtcg aagacattgt cctcaaggtg gctgctc   287

<210>   167
<211>   283
<212>   DNA
<213>   Zea mays

<400>   167

ccgcatctga atcggcactc ggcagcgcgc cactccatag tgtaggagga gatggcgctc   60

55

acaagaatcg gtcttgctgg ccttgcggtc atggggcaga accttgccct caacattgca   120

gagaaagggt tccccatctc tgtgtacaac aggacaacct ccaaggtgga cgagaccgtg   180

cagcgtgcca aggcagaagg aaaccttccc gtctacggct tccatgaccc cgcgtccttt   240

gtgaagtcca ttcagaagcc acgggtggtg atcatgctcg tca   283

<210>   168
<211>   285
<212>   DNA
<213>   Zea mays

<400>   168

ggtggacgag accgtgcagc gtgccaaggc agaaggaaac cttcccgtct acggcttcca   60

tgaccccgcg tcctttgtga agtccattca gaagccacgg gtggtgatca tgctcgtcaa   120

ggccggcgcg ccagttgacc agaccatcgc gacgctcgca gctcacttgg agcagggcga   180

ctgcatcatc gatggggga acgagtggta cgagaacacg gagatgaggg agaaggccat   240

ggaggatcgc ggcctcctgt atcttggcat gggtgtctct ggagg   285

<210>   169
<211>   311
<212>   DNA
<213>   Zea mays

<400>   169

gccggaggtg gtggcatcgc aattcaactc cgcatctgaa tcggcactcg gcagcgcgcc   60

actccatagt gtaggaggag gagatggcgc tcacaagaat cggtcttgct ggccttgcgg   120

tcatggggca gaaccttgcc ctcaacattg cagagaaagg gttccccatc tctgtgtaca   180

acaggacaac ctccaaggtg gacgagaccg tgcagcgtgc caaggcagaa ggaaaccttc   240

ccgtctacgg cttccatgac cccgcgtcct ttgtgaactc cattcagaag ccacgggtgg   300

tgatcatgct c   311

<210>   170
<211>   290
<212>   DNA
<213>   Zea mays

<400>   170

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aattcaactc cgcatctgaa tcggcactcg gcagcgcgcc agctccatag cgaggagatg    60

gcgctcacaa gaatcggtct tgctggcctt gcggtcatgg ggcagaacct tgccctcaac   120

attgcagaga tagggttccc catctctgtg tacaacagga caacctccaa ggtggacgag   180

accgtgcagc gtgccaaggc agaaggaaac cttcccgtct acggcttcca tgaccccgcg   240

tcctttgtga agtccattca gaagccacgg gtggtgatca tgctcgtcaa                290
```

```
<210>        171
<211>        275
<212>        DNA
<213>        Zea mays

<400>        171
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gctcgcagct cacttggagc agggcgactg catcatcgat gggggggaacg agtggtacga   120

gaacacggag aggagggaga aggccatgga ggagcgcggc ctcttgtatc ttggcatggg   180

tgtctctgga ggagaggagg gtgcccgcaa cggcccgtcc ttgatgcccg gatgctcgtt   240

cgacgcttac aagtacgtcg aagacattgt tctca                               275
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<210>        172
<211>        296
<212>        DNA
<213>        Zea mays

<400>        172
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ctcggcagcg cgccactcca tagtgtagga ggaggagatg gcgctcacaa gaatcggtct   120

tgctggcctt gcggtcatgg ggcagaacct tgccctcaac attgcagaga aagggttccc   180

catctctgtg tacaacagga caacctccaa ggtggacgag accgtgcagc gtgccaaggc   240

agaaggaaac cttcccgtct acggcttcca tgaccccgcg tcctttgtga actcca        296
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```
<210>        173
<211>        268
<212>        DNA
<213>        Zea mays

<400>        173
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```
gcgactgcat catcgatggg gggaacgagt ggtacgagaa cacggagagg agggagaagg     60

ccatggagga gcgcggcctc ttgtatcttg catgggtgt ctctggagga gaggagggtg    120

cccgcaacgg cccgtccttg atgcccggag ctcgttcga cgcttacaag tacgtcgaag    180

acattgttct caaggtggct gctcaggtcc ctgacagtgg cccgtgtgtc acgtacattg    240

gcaaaggtgg atcgggcaac tttgtcaa                                       268
```

```
<210>        174
<211>        276
<212>        DNA
<213>        Zea mays

<223>        unsure at all n locations
<400>        174
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```
acaagtacat tgaagatatt cttctcaagg tggctgctca ggtacctgac agcggcccgt     60

gcgtcacata tattggcaaa ggtggatcag gcaacttcgt caagatggtt cacaatggaa    120

ttgaatatgg tgacatgcaa cttatcgccg aggcttatga tgttctcaag ttcggtgggt    180

aagctcacaa acngcgagct gcatcaggtg ttctctgagt ggaacaaggg tgagctcctc    240

agtttcttga ttgagatcac ggccgacatc ttggta                             276
```

```
<210>        175
<211>        297
<212>        DNA
<213>        Zea mays

<400>        175
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cagcgcgcca gctccatagt gtaggaggag gtgatggcgc tcacaagaat cggtcttgct    120

ggccttgcgg tcatggggca gaaccttgcc ctcaacattg cagagaaagg gttccccatc    180

tctgtgtaca acaggacaac ctccaaggtg gacgagaccg tgcagcgtgc caaggcagaa    240

ggaaaccttc ccgtctacgg cttccatgac cccgcgtcct ttgtgaactc cattcag      297
```

```
<210>        176
<211>        274
<212>        DNA
<213>        Zea mays
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<223>   unsure at all n locations
<400>   176

acaagtacat tgaagatatt cttctcaagg tggctgctca ggtacctgac agcggcccgt   60

gcgtcacata tattggcaaa ggtggatcag gcaacttcgt caagatggtt cacaatggaa   120

ttgaatatgg tgacatgcaa cttatcgccg aggcttatga tgttctcaag tccggtgggt   180

aagctcacaa acngcgagct gcatcaggtg ttctctgagt ggaacaaggg tgagctcctc   240

agtttctgat tgagatcacg gccgacatct tggt   274

<210>   177
<211>   274
<212>   DNA
<213>   Zea mays

<400>   177

ggtggccgga cggtggtggc atcgccaatt caactccgca tctgaatcgg cactcggcag   60

cgcgccactc catagtgtag gaggagatgg cgctcacaag aatcggtctt gctggccttg   120

cggtcatggg gcagaacctt gccctcaaca ttgcagagaa agggttcccc atctctgtgt   180

acaacaggac aacctccaag gtggacgaga ccgtgcagcg tgccaaggca gaaggaaacc   240

ttcccgtcta cggcttccat gaccccgcgt cctt   274

<210>   178
<211>   271
<212>   DNA
<213>   Zea mays

<400>   178

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gcgcgccact ccatagtgta ggaggaggag atggcgctca caagaatcgg tcttgctggc   120

cttgcggtca tggggcagaa ccttgccctc aacattgcag agaaagggtt ccccatctct   180

gtgtacaaca ggacaacctc caaggtggac gagaccgtgc agcgtgccaa ggcagaagga   240

aaccttcccg tctacggctt ccatgacccc g   271

<210>   179
<211>   258
<212>   DNA
<213>   Zea mays

59

<400>   179

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gccaaggcag aaggaaacct tcccgtctac ggcttccatg accccgcgtc ctttgtgaac   120

tccattcaga agccacgggt ggtgatcatg ctcgtcaagg ccggcgcgcc agttgaccag   180

atcatcgcga cgctcgcagc tcacttggag cagggcgact gcatcatcga tggggggaac   240

gagtggtacg agaacacg   258

<210>   180
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<212>   DNA
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<400>   180

ggccggcgcg ccagttgacc agaccatcgc gacgctcgca gctcacttgg agcagggcga   60

ctgcatcatc gatggggggа acgagtggta cgagaacacg gagaggaggg agaaggccat   120

ggaggagcgc ggcctcttgt atcttggcat gggtgtctct ggaggagagg agggtgcccg   180

caacggcccg tccttgatgc ccggaggtcg ttcgacgctt acaagtacgt cgagacattg   240

ttctcaaggt ggctgctcag gtccctgaca   270

<210>   181
<211>   251
<212>   DNA
<213>   Zea mays

<400>   181

gtgatcatgc tcgtcaaggc cggcgcgcca gtagaccaga ccatcgcgac gctcgcagct   60

cacttggagc agggcgactg catcatcgat gggggaacg agtggtacga gaacacggag   120

aggagggaga aggccatgga ggagcgcggc ctcttgtatc ttggcatggg tgtctcttga   180

ggagaagaag gtgcccgcaa cggcccgtcc ttgatgcccg ggagctcgtt cgacgcttac   240

aagtacgtcg a   251

<210>   182
<211>   224
<212>   DNA
<213>   Zea mays

<400> 182

gccggaggtg gtggcatcgc caattcaact ccgcatctga atcggcactc ggcagcgcgc   60

cagctccata gtgtaggagg agatggcgct cacaagaatc ggtcttgctg gccttgcggt   120

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tcatggggca gaaccttgcc ctcaacattg cagagaaagg gttccccatc tctgtgtaca   180

acaggacaac ctccaaggtg gacgagaccg tggcacgtgc caaggcagaa ggaaa   235

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ctctgtgtac aacaggacaa cct   263

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cggaggtggc atcgccaatt caactccgca tctgaatcgg cactcggcag cgcgccagca   180

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63

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catcgcggag aaagggttcc ccatctcggt ctacaacagg acaacctcca aggttgatga   180

gaccgtgcag cgtgccaagg tcgaaggaaa cctcccagtg tttggtttcc acgaccccgc   240

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gtttggtttc cacgaccccg cgtccttcgt gagctccatc cagaagcccc gtgtcgtcat   240

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accagaccat tgccacgctc gcggcgcacc ttgatcaggg ggactgtatc gtcgatggtg   180

gcaacagtgg tacgagaaca cggagaagag ggagaaggcg atggaagagc gcgggctcct   240

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ccccatctcg gtctacaaca ggacaacctc caaggttgat gagaccgtgc agcgtgccaa   180

ggtcgaagga aacctcccag tgtttggttt ccacgacccc gcgtccttcg tgagctccat   240

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65

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tctcggtcta caacaggaca acctccaagg ttgatgagac cgtgcagcgt gccaaggtcg   240

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gacagaacct tgccctcaac atcgcggaga aagggttccc catctcggtc tacaacagga   180

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gatggctctc acgaggaatg gcctcgccgg cctcgcggtc atggacagaa ccttgccct   180

caacatcgcg gagaaagggt tccccatctc ggtctacaac aggacaacct ccaaggttga   240

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66

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cagaagcccc gtgtcgtcat catgctcgtc aaggctgggg cgccggtgga ccagaccatt   180

gccacgctcg cggcgcacct ggatcagggg gactgtatcg tcgatggtgg caacgagtgg   240

tacgagaaca cggagaggaa ggagaag   267

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acgagaattg gcctcgccgg cctcgcggtc atgggacaga accttgccct caacatcgcg   180

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cagcgtgcca aggtcgaagg aaacct   266

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cacgagaatt ggcctcgccg gcctcgcggt catgggacag aaccttgccc tcaacatcgc   180

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67

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ggagatggct ctcacgagaa tgcgcctcgc cggcctcgcg gtcatgggac agaaccttgc   180

cctcaacatc gcggagaaag ggttccccat ctcggtctac aacaggacaa cctccaaggt   240

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ccaaggttga tgagaccgtg cagcgtgcca aggtcgaagg aaacctcccc gtgtttggtt   120

tccacgaccc cgcgtccttc gtgagctccc atccagaagc cccgtgtcgt catcatgctc   180

gtcaaggctg gggcgccggt ggacc                                        205


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cgccgacaaa ggcctcctct acctcggcat gggcgtctcc ggcggcgaag acggcgcacg   180

ccacggcccc tccctcatgc ccggtgggtc ccaccaggcc tactccaacg tccaggacat   240

cctccacaaa atcgccgccc aggtcgacga                                    270


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tanctcggca tgggcgtctc cggcggcgaa gacggcgcac gccacggccc ctccctcatg   120
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69

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cccggtgggt cccaccatgc ctactccaac gtgccagnac atcct                      165


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tcggagggca agacttccgg caaaccttgt ccaggctcag agggacttgt ttggggcgca   180

tacttacgag agggttgatc gccctggggc ttttcatacc gagtggacga aactcgctcg   240

caatagtg                                                            248


<210>      213
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ggtttcggct gggattagta ctcccggaat gtgtgccagt cttgcttact ttgatatccta  120

tcggagggca agacttccgg caaaccttgt ccaggctcag agggacttgt ttggggcgca   180

tacttacgag agggttgatc gccctggggc ttttcatacc gagtggacga aactcgctcg   240

caatagtggg g                                                        251


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ttgggggagt tagctaggat tggaagggag ggtgcatcat aagggccgtg ttcttggacc   180

ggatcaagaa ggcttatcag aggaaccccta atttggcgag tttgattgtg gacccggagt   240
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70

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tcaaagagtg acatcatcgt gtccccttcg attctgtctg caaactttgc gaagcttggt   120

gatcaggtaa aagctgtgga ggtggcagga tgcgactgga ttcatgtcga tgtcatggac   180

gggcgctttg tgccaa   196

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<213>   Zea mays

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ctcaaagagt gatatcaggg tngtcccttc gcatctgtct ggaaactgtc gcaaagctat   120

gttgatcagg tagaagcgtg ggaggtggca agatgtgact ggattctgtc gatgtcatgg   180

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agaactgaga aggttatgtg cagagaaggg agtgaacccc tggattgagg ttgatggtgg   180

tgttggtccg aaaaatgcct acaaggttat tgaagctggc gcaaatgcca ttgtcgcagg   240

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cagcgagtcc ccgattttat caaggcaggt gctgatattg ttagtgtcca ctgtgaacag   120

acatcgacca tccatttgca ccgaacagtc aatcagatta aaagtctagg agcaaaggca   180

ggagttgttt tgaatccagc gactccactc actgcaattg attatgttct tgatgttgtt   240

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caagtaaaga aa   312

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gaacagacat cgaccatcca tttgcaccga acagtcaatc agattaaaag tctaggagca   120

aaggcaggag ttgttttgaa tccagcgact ccactcactg caattgatta tgttcttgat   180

gttgttgacc tggtgctgat tatgtctgtg aatcctgggt ttggtggcca gagctttatc   240

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ccctggattg aggt   314

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72

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ccactcactg caattgatta tgttcttgat gttgttgacc tggtgctgat tatgtctgtg   180

aatcctgggt ttggtggcca gagctttatc gagagtcaag taaagaaaat tgcagaactg   240

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ccgaa   305

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ctgattatgt ctgtgaatcc tgggtttggt ggccagagct ttatcgagag tcaagtaaag   180

aaaattgcag aactgagaag gttatgtgca gagaagggag tgaacccctg gattgaggtt   240

gatggtggtg ttggtccgaa aaatgcctac aaggttattg   280

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ttggttgttg atgctctgcg tccagtgact gatcttccgt tggatgtaca tctgatgatt   180

gtggaacctg agcagcgagt ccccgatttt atcaaggcag gtgctgatat tgttagtgtc   240

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73

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tggccagagc tttatcgaga gtcaggtaaa gaaaattg   218

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agaactgag   249

<210>   225
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gataaggtgc gcacactgag aaagaagtac ccttcccttg acatagaggt tgatggtggt   60

ctaggtcctt caaccataga cgtggccgca tctgctgggg ccaattgcat cgtcgctgga   120

agctctatat ttggcgctgc ggacccagga gccatcatat ctgtgctgag gaagagcgtc   180

gagggctctc agaacaaaaa ctgattttgg tgtttctgct gtaaagtact ccctccgttt   240

ttttttattc gtcgcgtttt agttcaaaca tgaactagcg gacgactgat attcgagaat   300

ggagggagta cttcga   316

<210>   226
<211>   301
<212>   DNA
<213>   Zea mays

<400>   226

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catcgtcgct ggaagctcta tatttggcgc tgcggaccca ggagccatca tatctgtgct  120

gaggaagagc gtcgagggct ctcagaacaa aaactgattt tggtgtttct gctgtaaagt  180

actccctccg ttttttttatt cgtcgcgttt tagttcaaac atgaactagc ggacgactga  240

tattcgagaa tggagggatt acttcgaccc tgcacgtcag atgagctgat cctcacattg  300

c                                                                  301


<210>    227
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<212>    DNA
<213>    Zea mays

<400>    227

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gactaacact gcagctatca aaggaataca gaccagccaa agacctctag ctgtagccgc  120

ataaggcgct ggacgtgtaa tcatttactc tgtgcaagtt taccagtgat gcgatctgta  180

tagttgtgtg tcttgtccaa ccatacgtat accgagatga aaagagacgg aggcagtgaa  240

gaactat                                                            247


<210>    228
<211>    319
<212>    DNA
<213>    Zea mays

<400>    228

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tcgcctccct gcggaccgcc tccatcggcc accccgcgg catcgcgtca tctacgccca  120

ggaaggcgtt ccaagtgagg gcatcagctc gggttgacaa gttctcaaag agtgatatca  180

ttgtgtcccc ttcgattctg tctgcaaact tcgccaagct tggtgatcag gtaaaagccg  240

tggaggtggc aggatgtgac tggattcatg tcgatgtcat ggacgggcgc tttgtgccaa  300

atatcacaat tggacctttt                                              319


<210>    229
<211>    301
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<212> DNA
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<400> 229

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cggaccgcct ccatcggcca cccccgtggc atcgcctcct ccacgcccag gaaggcattc   120

catgtgaggg catcagctcg ggttgacaaa ttctcaaaga gtgacatcat cgtgtcccct   180

tcgattctgt ctgcaaactt tgcgaacttg gtgatcaggt aaaagctgtg gaggtggcag   240

gatgcgactg gattcatgtc gatgtcatgg acgggcgctt tgtgccaaac atcacaattg   300

g   301

<210> 230
<211> 268
<212> DNA
<213> Zea mays

<400> 230

cgcagatggc gacgccgtcg tcgtcgcttt gctccagctt cgcctccctg cggaccgcct   60

ccatcggcca cccccgtggc atcgcctcct ccacgcccag gaaggcattc catgtgaggg   120

catcagctcg ggttgacaag ttctcaaaga gtgacatcat cgtgtcccct tcgattctgt   180

ctgcaaactt tgcgaacttc ggtgatcagg taaaagctgt ggaggtggca ggatgcgact   240

ggattcatgt cgatgtcatg gatgggcg   268

<210> 231
<211> 256
<212> DNA
<213> Zea mays

<400> 231

aagcgtcgtc gtcgctttgc tccagcttcg cctccctgcg gaccgcctcc atcggccacc   60

cccgtggcat cgcctcctcc acgcccagga aggcattcca tgtgagggca tcagctcggg   120

ttgacaaatt ctcaaagagt gacatcatcg tgtccccttc gattctgtct gcaaactttg   180

cgaagcttgg tgatcaggta aaagctgtgg aggtggcagg cggcgactgg attcatgtcg   240

atgtcatgga cgggcg   256

76

<210> 232
<211> 319
<212> DNA
<213> Zea mays

<400> 232

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gagaggcgcg cagatggcga cgccgtcgtc gtcgctttgc tccagcttcg cctccctgcg   120

gaccgcctcc atcggccacc cccgtggcat cgcctcctcc acgcccagga aggcattcca   180

tgtgagggca tcagctcggg ttgacaaatt ctcaaagagt gacatcatcg tgtccccttc   240

gattctgtct gcaaactttg cgaactctgg tgatcaggta aaagctgtgg aggtggcagg   300

atgcgactgg attcatgtc   319

<210> 233
<211> 287
<212> DNA
<213> Zea mays

<223> unsure at all n locations
<400> 233

ccagtggctg ctagccgaga cggggataga ttgacagaca ggcgcgcaga tcgcgacgcc   60

gtcgtcgtcg ctttgctcca gcttcgcctc cctgcggacc gcctccatcg gccaccccccg   120

tggcatcgcc tcctccacgc ccagtcaagg cattccatgt gagggcatca gctcgggttc   180

acaaattctc aaagagtgac atcatcgtgt ccccttcgat tctgtctgca actttgcga   240

acttggtgat caggtanaag ctgtggaggt ggcaggatgc gactgga   287

<210> 234
<211> 261
<212> DNA
<213> Zea mays

<400> 234

agaggggata gattgagaga gccagagagg tgggcagatg gcgacaccgt cgtcgtcgct   60

ttgctccagc ttcgcctccc tgcggaccgc ctccatcggc caccccgcg gcatcgcgtc   120

atctacaccc aggaaggcgt tccaagtgag ggcatcagct cgggttgaca agttctcaaa   180

gagtgatatc attgtgtccc cttcgattct gtctgcaaac ttcgccaagc ttggtgatca   240

77

ggtaaaagcc gtggaggtgg c   261

<210>   235
<211>   299
<212>   DNA
<213>   Zea mays

<400>   235

gctcttgcaa caagccaaac aacccagtgg ctgctagccg agacagggga tagattgaga   60

gagaggcgcg cagatggcga cgccgtcgtc gtcgctttgc tccagcttcg cctccctgcg   120

gaccgcctcc atcggccacc cccgtggcat cgcctcctcc acgcccagga aggcattcca   180

tgtgagggca tcagctcggg ttgacaaatt ctcaaagagt gacatcatcg tgtccccttc   240

gattctgtct gcaaactttg cgaacgttgg tgatcaggta aaagctgtgg aggtggcag   299

<210>   236
<211>   241
<212>   DNA
<213>   Zea mays

<400>   236

attgacagac aggcgcgcag atggcgacgc cgtcgtcgtc gctttgctcc agcttcgcct   60

ccctgcggac cgcctccatc ggccaccccc gtggcatcgc ctcctccacg cccaggaagg   120

cattccatgt gagggcatca gctcgggttg acaaattctc aaagagtgac atcatcgtgt   180

ccccttcgat tctgtctgca aactttgcga agcttggtga tcaggtaaaa gctgtggagg   240

t   241

<210>   237
<211>   293
<212>   DNA
<213>   Zea mays

<400>   237

ctcttgcaac aagccaaaca acccagtggc tgctagccga gacaggggat agattgagag   60

agaggcgcgc agatggcgac gccgtcgtcg tcgctttgct ccagcttcgc ctccctgcgg   120

accgcctcca tcggccaccc ccgtggcatc gcctcctcca cgcccaggaa ggcattccat   180

gtgagggcat cagctcgggt tgacaaattc tcaaagagtg acatcatcgt gtccccttcg   240

78

attctgtctg caaactttgc gaactgtggt gatcaggtaa aagctgtgga ggt   293

<210>   238
<211>   325
<212>   DNA
<213>   Zea mays

<400>   238

accaaatcgc ttaccgcccc cgaagcgtct cggttcgcat agcagagctg ctcttgcaac   60

aagccaaaca acccagtggc tgctagccga gacaggggat agattgagag agaggcgcgc 120

agatggcgac gccgtcgtcg tcgctttgct ccagcttcgc ctccctgcgg accgcctcca 180

tcggccaccc ccgtggcatc gcctcctcca cgcccaggaa ggcattccat gtgagggcat 240

cagctcgggt tgacaaattc tcaaagagtg acatcatcgt gtccccttcg attctgtctg 300

caaactttgc gaacgttggt gatca   325

<210>   239
<211>   301
<212>   DNA
<213>   Zea mays

<400>   239

cgaagctctc ggttcgcata gcagagctgc tcttgcaaca agccaaacaa cccagtggct   60

gctagccgag acaggggata gattgagaga gaggcgcgca gatggcgacg ccgtcgtcgt 120

cgctttgctc cagcttcgcc tccctgcgga ccgcctccat cggccacccc gtggcatcg 180

cctcctccac gcccaggaag ggattccatg tgagggcatc agctcgggtt gacaaattct 240

caaagagtga catcatcgtg tccccttcga ttctgtctgc aaactttgcg aagcttggtg 300

a   301

<210>   240
<211>   288
<212>   DNA
<213>   Zea mays

<400>   240

agcagagctg ctcttgcaac aagccaaaca acccagtggc tgctagccga gacaggggat   60

agattgagag agaggcgcgc agatggcgac gccgtcgtcg tcgctttgct ccagcttcgc 120

79

```
ctccctgcgg accgcctcca tcggccaccc ccgtggcatc gcctcctcca cgcccaggaa    180

ggcattccat gtgagggcat cagctcgggt tgacaaattc tcaaagagtg acatcatcgt    240

gtccccttcg attctgtctg caaactttgc gaactgtggt gatcaggt                 288


<210>      241
<211>      304
<212>      DNA
<213>      Zea mays


<400>      241

aatcgcttac cgccccgaa gcgtctcggt tcgcatagca gagctgctct tgcaacaagc     60

caaacaaccc agtggctgct agccgagaca ggggatagat tgagagagag gcgcgcagat    120

ggcgacgccg tcgtcgtcgc tttgctccag cttcgcctcc ctgcggaccg cctccatcgg    180

ccaccccgt ggcatcgcct cctccacgcc caggaaggca ttccatgtga gggcatcagc     240

tcgggttgac aaattctcaa agagtgacat catcgtgtcc ccttcgattc tgtctgcaaa    300

cttt                                                                 304


<210>      242
<211>      229
<212>      DNA
<213>      Zea mays

<223>      unsure at all n locations
<400>      242

cataactact ctgccaccaa tccggggagg aatcaaccta gcggtaagcg gacatggcgg     60

cggcgaagat agcgccgtcg atgctctcgt cggactttgc caacctcgct tcggaggctg    120

agcgcatggt ccgcctaggc gccgactggc tacatatgga catcatggat gggcacttcg    180

ttcctaacct gactattggg gctccggtga tccagangct tgagaaata                229


<210>      243
<211>      269
<212>      DNA
<213>      Zea mays


<400>      243

gctacatatg gacatcatgg atgggcactt cgttcctaac ctgactattg gggctccggt     60

gatccagagc ttgaggaaac ataccaaagc atatttggac tgccatctta tggtcacaaa    120
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80

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gccttcagat tacgtagaac catttggaaa ggctggcgct tctggattca cattccatat   180

agaagttgct agagacaact ggcaagatct catccaaagc attaaatcaa agggtatgcg   240

gcctggtgta tcattgaggc caggtactc                                      269


<210>      244
<211>      385
<212>      DNA
<213>      Zea mays

<400>      244

ccgggctcaa ccaacgcgtc aggatgtttt gaaccaacca acccaatcaa cggaaattga    60

taacttcctg gaggtggttg acctgtggcg dataaggtcg gtaaacccgg ggttgggggg   120

caaaacctta accaaaagtc aattaaagaa aattgcaaaa ctgaaaaggt aatgtgcaaa   180

aaagggagtg aacccoggga ttgaggttga tggtggtgtt ggtccgaaaa atgcctacaa   240

ggttattgaa gctggcgcaa atgccattgt cgcaagttct gcagtttttg gggctccaga   300

ctacgctgaa gctatcaaag gaataaagac cagccaaaga cctctagctg tagccgcata   360

aagagctgga cgtgtaatca tttac                                         385


<210>      245
<211>      389
<212>      DNA
<213>      Zea mays

<223>      unsure at all n locations
<400>      245

gaccaagccg tccaatcaag gtggaggcca tggatgggcc ctttgtgcca aacatcacaa    60

ttggaccctg gggtgttgat gctctgcgtc cagtgactga tcttccgttg gatgtacatc   120

tgatgattgt ggaacctgag cagcgagtcc ctgattttat caaggcaggt gctgatattg   180

ctagtgtcca ctgtgaacag acatcgacct tcatttgcac cgaacagtca atcagattaa   240

aagtctagga gcanaggcag ggattgttnt gaatccagcg actccactca ctgcaattga   300

ttacgttctt gatgttgttg acctggtgct gattatgtct gtgaatcctg ggtttgttgg   360

cagagcttta tcgagagtca agtaaggaa                                      389


<210>      246
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81

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<211>        412
<212>        DNA
<213>        Zea mays

<400>        246

gtgtcccctt cgattctgtc tgcaaacttt gcgaagcttg gtgatcaggt aaaagctgtg    60

gaggtggcag gatgcgactg gattcatgtc gatgtcatgg acgggcgctt tgtgccaaac   120

atcacaattg gacccttggt tgttgatgct ctgcgtccag tgactgatct tccgttggat   180

gtacatctga tgattgtgga acctgagcag cgagtccccg attttatcaa ggcaggtgct   240

gatattgtta gtgtccactg tgaacagaca tcgaccatcc atttgcaccg aacagtcaat   300

cagattaaaa gtctaggagc aaaggcagga gttgttttga atccagcgac tccactcact   360

gcaattgatt acgttcttga tgttgttgac ctggtgctga ttatgtctgt ga           412


<210>        247
<211>        397
<212>        DNA
<213>        Zea mays

<400>        247

gatgctctgc gtccagtgac tgatcttccg ttggatgtac atctgatgat tgtggaacct    60

gagcagcgag tccctgattt tatcaaggca ggtgctgata ttgttagtgt ccactgtgaa   120

cagacatcga ccatccattt gcaccgaaca gtcaatcaga ttaaaagtct aggagcaaag   180

gcaggagttg ttttgaatcc agcgactcca ctcactgcaa ttgattacgt tcttgatgtt   240

gttgacctgg tgctgattat gtctgtgaat cctgggtttg gtggccagag ctttatcgag   300

agtcaagtaa agaaaattgc agaactgaga aggttatgtg cagagaaggg agtgaacccc   360

tggattgagg ttgatggtgg tgttggtccg aaaaatg                            397


<210>        248
<211>        403
<212>        DNA
<213>        Zea mays

<400>        248

ggaggtggca ggatgcgact ggattcatgt cgatgtcatg gacgggcgct ttgtgccaaa    60

catcacaatt ggacccttgg ttgttgatgc tctgcgtcca gtgactgatc ttccgttgga   120
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82

```
tgtacatctg atgattgtgg aacctgagca gcgagtcccc gattttatca aggcaggtgc    180

tgatattgtt agtgtccact gtgaacagac atcgaccatc catttgcacc gaacagtcaa    240

tcagattaaa agtctaagag caaaggcagg gaattgtttg aatccagcga cttcacttac    300

tggaattgat tatggtcctg atggtggtga cctggtgctg attatgtctg tgaatcctgg    360

gtttggtggc caaagcttta ttgagagtca agttaaggaa att                      403
```

```
<210>      249
<211>      419
<212>      DNA
<213>      Zea mays

<223>      unsure at all n locations
<400>      249
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gtgaaagccg tggaggtggc aggatgttac tggattcatg tcgatgtcat ggacgggcgc    60

tttgtgccaa atatcacaat tggacctttg gttgttgatg ctctgcgtcc tgtgactgat    120

cttccattgg atgtacatct gatgattgtg gaacctgagc agcgagtccc tgattttatc    180

aaggcaggtg ctgatattgt tagtgtccac tgtgaacaaa catcgaccat ccatttgcac    240

agaacagtca atcagattaa aagtctagga gcaaaagcag gagttgtttt gaatccagcg    300

actccactca atgcaattga ttacattctt gatgttgttg acctggtgtt gattatgtct    360

gtgaatcctg ggtttggtgg ccagagcttt atcgagagtc aagtnaggaa aattgcaga    419
```

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<210>      250
<211>      451
<212>      DNA
<213>      Zea mays

<400>      250
```

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tctgcgtcca gtgactgatc ttccgttgga tgtacatctg atgattgtgg aacctgagca    120

gcgagtcccc gattttatca aggcaggtgc tgatattgtt agtgtccact gtgaacagac    180

atcgaccatc catttgcacc gaacagtcaa tcagattaaa agtctaggag caaaggcagg    240

agttgttttg aatccagcga ctccactcac tgcaattgat tatgttcttg atgttgttga    300

cctggtgctg attatgtctg tgaatcctgg gtttggtggc cagagcttta tcgagagtca    360

agtaaagaag attgcagaac tgagaaggtt atgtgcagag aagggagtga accccctggat    420
```

83

```
tgaggttgat ggtggtgttg gtcccaaaaa t                            451


<210>       251
<211>       389
<212>       DNA
<213>       Zea mays

<400>       251

cttggtgatc aggtaaaagc tgtggaggtg gcatgatgcg actggattca tgttgatgtc   60

atggatgggc gctttgtggc aaacatcaca attggaccct tggttgttga tgctctgcgt  120

ccagtgactg atcttccgtt ggatgtacat ctgatgattg tggaacctga gcagcgagtc  180

cctgatttta tcaaggcagg tgctgatatt gatagtgtcc actgtgaaca gacatcgacc  240

attcatttgc accgaacagt caatcagatt aaaagtctat gagcaaaggc aggagttgtt  300

gtgaatccag cgactgcact cactgcaatt gattacgttc ttgatgatga tgacctggtg  360

ctgattatgt ctgtgaatcc tgggtttgg                                    389


<210>       252
<211>       426
<212>       DNA
<213>       Zea mays

<400>       252

ctatgaacag acatcgacca tccatttgca ccgaacaatc aatcagatta aaagtctagg   60

agcaaaggca ggagttgttt tgaatccagc gactccactc actgcaattg attaggggct  120

tgatgttgtt gacctggtgc tgattagggg ggtgaatcct gcgtttggtg gccagagctt  180

tatcgagagt caagtaaaga aaattgcaga actgagaagg ttatgtgcag agaagggagt  240

gaacccctgg attgaggttg atggtggtgt tggtccgaaa aatgcctaca aggttattga  300

agctggcgca aattctattt tctcaggttc tgcagttttt ggggctccag actacgctga  360

agctatcaaa tggaataaga ccatccaaag acctctagct gtagccgcat aaacaacttg  420

acgtgt                                                             426


<210>       253
<211>       380
<212>       DNA
<213>       Zea mays
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84

<400> 253

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cggacgcgtg ggcggacgcg tgggctgaga aggttatgtg cagagaaggg agtgaacccc   60

tggattgagg ttgatggtgg tgttggtccg aaaaatgcct acaaggttat tgaagctggc  120

gcaaatgcca ttgtcgcagg ttctgcagtt tttggggctc cagactacgc tgaagctatc  180

aaaggaataa agaccagcca aagacctcta gctgtagccg cataaggagc tggacgtgta  240

atcatttact ctgtgcaagt ttaccagtga tgcgatctgt atagatgtgt gtcttgtcca  300

gccatacgta taccggagat gaaaagagac ggaagcagtg aagaaatatc cttttttttt  360

cttctcattt ttcacgaaga                                              380
```

<210>   254
<211>   375
<212>   DNA
<213>   Zea mays

<400>   254

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agagagccag agaggtgggc agatggcgac accgtcgtcg tcgctttgct ccagcttcgc   60

ctccctgcgg accgcctcca tcggccaccc ccgcggcatc gcgtcatcta cgcccaggaa  120

ggcgttccaa gtgagggcat cagctcgggt tgacaagttc tcaaagagtg atatcattgt  180

gtccccttcg attctgtctg caaacttcgc caagcttggt gatcaggtaa aagccgtgga  240

ggtggcagga tgtgactgga ttcatgtcga tgtcatggac gggcgctttg tgccaaatat  300

cacaattgga cctttggttg ttgatgctct gcgtcctgtg actgatcttc cattggatgt  360

acatctgatg attgt                                                   375
```

<210>   255
<211>   429
<212>   DNA
<213>   Zea mays

<400>   255

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cacacgcgtc cgcaacaagc caaacaaccc agtggctgct agccgagaca ggggatagat   60

tgagagagag gcgcgcagat ggcgacgccg tcgtcgtcgc tttgctccag cttcgcctcc  120

ctgcggaccg cctccatcgg ccaccccgt ggcatcgcct cctccacgcc caggaaggca  180

ttccatgtga gggcatcagc tcgggttgac aaattctcaa agagtgacat catcgtgtcc  240
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85

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ccttcgattc tgtctgcaaa ctttgcgaag cttggtgatc aggtaaaagc tgtggaggtg   300

gcaggatgcg actggattca tgtcgatgtc atggacgggc gctttgtgcc aaacatcaca   360

attggacccct tggttgttga tgctctgcgt ccagtgactg atcttccgtt ggatgtacat   420

ctgatgatg                                                             429


<210>      256
<211>      424
<212>      DNA
<213>      Zea mays

<400>      256

atcgcttacc gcccccgaag cgtctcggtt cgcatagcag agctgctctt gcaacaagcc    60

aaacaaccca gtggctgcta gccgagacag gggatagatt gagagagagg cgcgcagatg   120

gcgacgccgt cgtcgtcgct ttgctccagc ttcgcctccc tgcggaccgc ctccatcggc   180

cacccccgtg gcatcgcctc ctccacgccc aggaaggcat tccatgtgag ggcatcagct   240

cgggttgaca aattctcaaa gagtgacatc atcgtgtccc cttcgattct gtctgcaaac   300

tttgcgaagc ttggtgatca ggtaaaagct gtggaggtgg caggatgcga ctggattcat   360

gtcgatgtca tggacgggcg ctttgtgcca aacatcacaa ttggacccct tggttgttgat   420

gctc                                                                  424


<210>      257
<211>      419
<212>      DNA
<213>      Zea mays

<223>      unsure at all n locations
<400>      257

cgcccccgaa gcgtctcggt tcgcatagca aagctgctct tgcaacaagc caaacaaggc    60

antggctgct agccgagaca ggggatagat tgagagagag gcgcgcagat ggcgacgccg   120

tcgtcgtcgc tttgctccag cttcgcctcc ctgcggaccg cctccatcgg ccacccccgt   180

ggcatcgcct cctccacgct caggaaggca ttccatgtga gggcatcagc tcgggttgac   240

aagttctcaa agagtgacat catcgtgtcc ccttcgattc tgtctgcaaa ctttgcgaag   300

cttggtgatc aggtaaaagc tgtggaggtg gcaggatgcg actggattca tgtcgatgtc   360
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86

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atggacgggc gctttgtgcc aaacatcaca attggaccct ggtttgtga tgctctgcg    419
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<210>        258
<211>        416
<212>        DNA
<213>        Zea mays
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<400>        258
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aacaagccaa acaacccagt ggctgctagc cgagacaggg gatagattga gagagaggcg   120

cgcagatggc gacgccgtcg tcgtcgcttt gctccagctt cgcctccctg cggaccgcct   180

ccatcggcca cccccgtggc atcgcctcct ccacgctcag gaaggcattc catgtgaggg   240

catcagctcg ggttgacaag ttctcaaaga gtgacatcat cgtgtcccct tcgattctgt   300

ctgcaaactt tgcgaagctt ggtgatcagg taaaagctgt ggaggtggca ggatgcgact   360

ggattcatgt cgatgtcatg gacgggcgct ttgtgccaaa catcacaatt ggaccc        416
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<210>        259
<211>        390
<212>        DNA
<213>        Zea mays
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```
<223>        unsure at all n locations
<400>        259
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gcgcagatgg cgacgccgtc gtcgtcgctt tgctccagct tcgcctccct gcggaccgcc   120

tccatcggcc acccccgtgg catcgcctcc tccacgccca ggaaggcatt ccatgtgagg   180

gcatcagctc gggttgacaa attctcaaag agtgacatca tcgtgtcccc ttcgattctg   240

tctgcaaact ttgcgaagct tggtgatcag gtaaaagctg tggaagtggc aggatgcgac   300

tggattcatg tcgatgtcat ggacgggcgc tttgtgccaa acatcacaat tggacccttg   360

ngttgtgatg ctctgcgtcc agtgactgat                                      390
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```
<210>        260
<211>        415
<212>        DNA
<213>        Zea mays
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<400>        260
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gttttgtttg ttgtccgcct ggcgcctggc cccataacta ctctgccaca atccggggaa   60

gaatcaacct agcggtaagc ggacatggcg gcggcgaaga tagcgccgtc gatgctctcg   120

tcggactttg ccaacctcgc ttcggaggct gagcgcatgg tccgcctagg cgccgactgg   180

ctacatatgg acatcatgga tgggcacttc gttcctaacc tgactattgg ggctccggtg   240

atccagagct tgaggaaaca taccaaagca tatttggact gccatcttat ggtcacaaag   300

ccttcagatt acgtagaacc atttggaaag gctggcgctt ctggattcac attccatata   360

gaagttgcta gagacaactg gcaagatctc atccaaagca ttaaatcaaa gggta   415

<210>   261
<211>   257
<212>   DNA
<213>   Glycine max

<400>   261

aaaatttcaa ccacagtgaa ggctacatct cgtgttgaca agttttcaaa aagcgatatc   60

attgtctctc catccattct ttctgcaaac tttgcaagat tgggacaaca ggtgaaagca   120

ctgcagttgg ctggttgtga ttggcttcac gttgatgtaa tggatggccg ttttgttcca   180

aatattacaa ttggacctct tgtcggctga tgcattgcgc cctgtgacag atcttccttt   240

ggatgtacac ctgatga   257

<210>   262
<211>   272
<212>   DNA
<213>   Glycine max

<223>   unsure at all n locations
<400>   262

gggagttgaa aganagaaag gaaggatggg agtgacaccg aaaattgctc cttcgatgct   60

ctcttccgac ttcgccaatt tggcttccga ggctcagcgc atgctccact tcggcgccga   120

ttggctccac atggacatca tggatgggca ttttgtcccc aatttaacta ttggcgctcc   180

agttattgaa agtttgagaa agcacacaaa gggatatttg gattgtcacc ttatggttac   240

aaatcctctt gattatgttg agnccttggc aa   272

<210>   263

<211>   260
<212>   DNA
<213>   Glycine max

<223>   unsure at all n locations
<400>   263

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ttccgacttc gccaatttgg cttccgaggc tcagcgcatg ctccacttcg gcgccgattg   120

gctccacatg gacatcatgg atgggcattt tgtccccaat ttaactattg gcgctccagt   180

tattgaaagt ttgagaaagc acacaaaggg atatttggat tgtcacctta tggttacaaa   240

tcctcttgat tatgttgagc                                               260
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<210>   264
<211>   266
<212>   DNA
<213>   Glycine max

<400>   264

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caaggaagga tgggagtgac accgaaaatt gctccttcga tgctctcttc cgacttcgcc    60

aatttggctt ccgaggctca gcgcatgctc cacttcggcg ccgattggct ccacatggac   120

atcatggatg ggtcttttgt ccccaattta actattggcg ctccagttat tgaaagtttg   180

agaaagcaca caaagggata tttggattgt caccttatgg ttacaaatcc tcttgattat   240

gttgagccct tggcaaaagc tggtgc                                        266
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<210>   265
<211>   228
<212>   DNA
<213>   Glycine max

<223>   unsure at all n locations
<400>   265

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tgacaccgaa aattgctcct tcgatgctcn cttccgantt cgcnaatttg gcttccgagg    60

ctcagcgcat gctccacttc ggcgccgatt ggctccacat ggacatcatg gntgggnatt   120

ttgtccccaa tttaactatt ggcgctccag ttattganag tttgagaaag cacacaaagg   180

gatatttnng attgtcacct tatggttaca aatcctcttg attatgtt               228
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<210>   266
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<211>        243
<212>        DNA
<213>        Glycine max

<400>        266

caaccataga tgtggccgca tcagcagggg caaactgcat tgttgctgga agttcagtgt    60

ttggtgcccc tgagccagtt caagtaatat ccttactaag gaattctgtt gagaaagccc   120

agcaaacctt gatacagtaa aaaaaaaatg tcgttttaag ttgcagtaca cttcacaact   180

ttgcataaac aatatgctta atgtttaaca ttttccataa gttgaataaa agatcatgtg   240

act                                                                 243


<210>        267
<211>        266
<212>        DNA
<213>        Glycine max

<400>        267

agaggttgat ggtggtttag ggccttcaac catagacgtg ccgcatcag cagggcaaa    60

ttgcattgtt gctggaagtt ctgtttttgg tgcacctgag ccagctcaag taatatccta   120

ctgaggagtt ctgttgagaa agcccagcaa acctcgatac agtaaaacaa tgtcgtttta   180

agttgcagta tacttcacaa ctttacataa acaatatgct aatgttaaca tttcataagt   240

tgaataaaag atcaagtgct tgaaaa                                        266


<210>        268
<211>        229
<212>        DNA
<213>        Glycine max

<400>        268

gaaaatttct gacttgagaa gagtgtgcgc ggaaaaggga gtgaatccat ggattgaagt    60

agatggtgga gttggtccag caaatgctta caaggtgatt gaggctggag ccaatgctct   120

ggttgcaggc tctgcttgtt tggagctaaa gattatgccg aagctataag aggaatcaaa   180

accagcaaaa gacctgaagc agttgctgtg tgaaatgccc atgtggttc                229


<210>        269
<211>        266
<212>        DNA

<213>      Glycine max

<400>      269

cccccatccc caccccaact tgtatattgt gcataatatc tatctgcatt ctctctcttc      60

agggagtgaa tccatggatt gaagtagatg gtggagttgg tccagcaaat gcttacaagg     120

tgattgaggc tggagccaat gctctggttg caggctctgc tgtgtttgga gctaaagatt     180

atgccgaagc tataagagga atcaaaacca gcaaaagacc tgaagcagtt gctgtgtgaa     240

atgcccatgt ggttcaatat tcaccg                                          266


<210>      270
<211>      257
<212>      DNA
<213>      Glycine max

<400>      270

agcgatatca ttgtctctcc gtccattctt tctgcaaact tttcaaaatt gggagagcag      60

gtgaaagcag tggaattggc tggttgtgat tggattcacg ttgatgtaat ggatggtcgc     120

tttgttccaa atattacaat tggacctctt gtggttgatg cattgcgccc tgtgacagat     180

cttcctttgg atgtacacct gatgattgta gacctgaaca aagggtacca gattttatta     240

aggcaggagc tgatata                                                    257


<210>      271
<211>      274
<212>      DNA
<213>      Glycine max

<223>      unsure at all n locations
<400>      271

caagtttca aaaagcgata tcattgtttc tccatccatt ctttctgcaa actttgcaaa      60

attgggganag cangtgaaag cagtggagtn gnnggntggt aatnggntca angtngatgt     120

aatggatggc cngtttngtn ccaaatatta caattggacc tcttgtggtt gatgcattgc     180

cgcccctgtg acagatcttc cttnggatgt acacctgatg attgtagacc ctgaacaaag     240

ggtaccagat tttattaagg caggagcccg atac                                 274


<210>      272
<211>      281

<212>        DNA
<213>        Glycine max

<223>        unsure at all n locations
<400>        272

cttcttcctt gtgttcatcg accctccaat cccaaatcaa tggattctgc cttcacaaaa    60

cctctctttc ccatcctcgt tccctcactt tctccaggaa gaaaatttca accacagtga   120

aggctacatc tcgtgttgac aagttttcaa aaagcgatat cattgtttct ccatccattc   180

tttctgcaaa ctttgcaaaa ttgggagagc aggtgaaagc agtggagttg gctggttntg   240

atggattcac gttgatgtaa tggatgggcg tttgttccaa a                       281


<210>        273
<211>        256
<212>        DNA
<213>        Glycine max

<400>        273

gatggctgca acctcttcct tgtgctcatc gaccctccaa tcccagatca atggattctt    60

ccttcacaaa acctctcttt cccatactcc ttccctcact ttctccagga ggaaaatttc   120

aaccacagtg aaggctacat ctcgagtcga caagttttca aaaagcgata tcattgtctc   180

tccgtccatt ctttctgcaa acttttcaaa attggagagc aagtgaaagc agtagaattg   240

gctggttgtg attgga                                                   256


<210>        274
<211>        273
<212>        DNA
<213>        Glycine max

<223>        unsure at all n locations
<400>        274

gattgctgag tcaaacttga attgaaggtg aagaaggaga tggcagnaac ttcttccttg    60

tgttnatcga ncctncaatc ccaaatcaat ggattctgcn ttcacaaaac ctctntttcc   120

catcctcgtt ccctnacttt ctcnaggaag aaaatttcaa ccacagtgaa ggctacatct   180

cgtgttnaca agttttcaaa aagcgatatc attgtttctc catccattct ttntgcaaac   240

tttgcaaaat tgggagagca ggtgaaagca gtg                                273

<210> 275
<211> 260
<212> DNA
<213> Glycine max

<223> unsure at all n locations
<400> 275

ggtnangtaa acttganttg aagtgaagaa ggagatggct gcaacctctt ccttgtgctt    60

catcgaccct ccaatcccag atcaatggat tcttccttca caaaacctct ctttcccata   120

ctccttccct cactttctcc aggaggaaaa tttcaaccac agtgaaggct acatctcgag   180

tcgacaagtt ttcaaaaagc gatatcattg tctctccgtc cattctttct gcaactttt    240

caaaattggg agagcaggtg                                               260


<210> 276
<211> 247
<212> DNA
<213> Glycine max

<400> 276

gtcaaacttg aattgaaggt gaagaaggag atggcagcaa cttcttcctt gtgttcatcg    60

accctccaat cccaaatcaa tggattctgc cttcacaaaa cctctctttc catcctcgt    120

tccctcactt tctccaggaa gaaaatttca accacagtga aggctacatc tcgtgttgac   180

aagttttcaa aaagcgatat cattgtttct ccatccattc tttctgcaaa ctttgcaaaa   240

ttgggag                                                             247


<210> 277
<211> 255
<212> DNA
<213> Glycine max

<400> 277

ggattggtga ggtaaacttg aattgaagtg aagaaggaga tggctgcaac ctcttccttg    60

tgctcatcga ccctccaatc ccagatcaat ggattcttcc ttcacaaaac ctctctttcc   120

catactcctt ccctcacttt ctccaggagg aaaatttcaa ccacagtgaa ggctacatct   180

cgagtcgaca agttttcaaa aagcgatatc attgtctctc cgtccattct ttctgcaaac   240

ttttcaaaat tggga                                                    255

<210>     278
<211>     254
<212>     DNA
<213>     Glycine max

<400>     278

cgattggtga ggtaaacttg aattgaagtg aagaaggaga tggctgcaac ctcttccttg    60

tgctcatcga ccctccaatc ccagatcaat ggattcttcc ttcacaaaac ctctctttcc   120

catacttctt ccctcacttt ctccaggagg aaaatttcaa ccacagtgaa ggctacatct   180

cgagtcgaca agttttcaaa aagcgatatc attgtctctc cgtccattct ttctgcaaac   240

ttttcaaaat tggg                                                     254


<210>     279
<211>     276
<212>     DNA
<213>     Glycine max

<400>     279

gcataggatt ggtgaggtaa acttgaattg aagtgaagaa ggagatggct gcaacctctt    60

ccttgtgctc atcgaccctc caatcccaga tcaatggatt cttccttcac aaaacctctc   120

tttcccatac tccttccctc actttctcca ggaggaattt caaccacagt gaaggctaca   180

tctcgagtcg acaagttttc aaaaagcgat atcattgtct ctccgtccat tctttctgca   240

aacttttcaa aattgggaga gcaggtgaaa gcagtg                             276


<210>     280
<211>     244
<212>     DNA
<213>     Glycine max

<400>     280

taggattggt gaggtaaact tgaattgaag tgaagaagga gatggctgca acctcttcct    60

tgtgctcatc gaccctccaa tcccagatca atggattctt ccttcacaaa acctctcttt   120

cccatactcc ttccctcact ttctccagga ggaaaatttc aaccacagtg aaggctacat   180

ctcgagtcga caagttttca aaaagcgata tcattgtctc tccgtccatt ctttctgcaa   240

actt                                                                244


94

<210>     281
<211>     249
<212>     DNA
<213>     Glycine max

<400>     281

cttttgtgaa ggcctaggat tgctgagtca aacttgaatt gaaggtgaag aaggagatgg     60

cagcaacttc ttccttgtgt tcatcgaccc tccaatccca aatcaatgga ttctgccttc    120

acaaaacctc tctttcccat cctcgttccc tcactttctc caggaagaaa atttcaacca    180

cagtgaaggc tacatctcgt gttgacaagt tttcaaaaag cgatatcatt gtttctccat    240

ccattcttt                                                            249


<210>     282
<211>     262
<212>     DNA
<213>     Glycine max

<400>     282

cacacacttt tttcaaggca taggattggt gaggcaaact tgaattgaag tgaagaagga     60

gatggctgca acctcttcct tgtgctcatc gaccctccaa tcccagatca atggattctt    120

ccttcacaaa acctctcttt cccatactcc ttccctcact ttctccagga ggaaaatttc    180

aaccacagtg aaggctacat ctcgagtcga caagttttca aaaagcgata tcattgtctc    240

tccgtccatt ctttctgcaa at                                             262


<210>     283
<211>     249
<212>     DNA
<213>     Glycine max

<400>     283

ttttgtcaag gcataggatt ggtgaggtaa acttgaattg aagtgaagaa ggagatggct     60

gcaacctctt ccttgtgctc atcgaccctc caatcccaga tcaatggatt cttccttcac    120

aaaaccttct ttcccatact ccttccctca ctttctccag gaggaaaatt tcaaccacag    180

tgaaggctac atctcgagtc gacaagtttt caaaaagcga tatcattgtc tctccgtcca    240

ttctttctg                                                            249


95

<210>		284
<211>		265
<212>		DNA
<213>		Glycine max

<400>		284

cacacagtca cactttgtg aaggcctagg attgctgagt caaacttgaa ttgaaggtga		60

cgaaggagat ggcagcaact tcttccttgt gttcatcgac cctccaatcc caaatcaatg		120

gattctgcct tcacaaaacc tctctttccc atcctcgttc cctcactttc tccaggaaga		180

aaatttcaac cacagtgaag gctacatctc gtgttgacaa gttttcaaaa agcgatatca		240

ttgtttctcc atccattctt tctgc		265


<210>		285
<211>		250
<212>		DNA
<213>		Glycine max

<400>		285

caaggcatag gatcggtgag gcaaacttga attgaagtga agaaggagat ggctgcaacc		60

tcttccttgt gctcatcgac cctccaatcc cagatcaatg gattcttcct tcacatcacc		120

tctcttcccc atactccttc cctcactttc tccaggagga aaatttcaac cacagtgaag		180

gctacatctc gagtcgacaa gttttcaaaa agcgatatcat tgtctctccg tccattcttt		240

ctgcaaattt		250


<210>		286
<211>		251
<212>		DNA
<213>		Glycine max

<400>		286

cacactttg tcaaggcata ggattggtga ggtaaacttg aattgaagtg aagaaggaga		60

tggctgcaac ctcttccttg tgctcatcga ccctccaatc ccagatcaat ggattcttcc		120

ttcacaaaac ctctctttcc catactcctt ccctcacttt ctccaggagg aaaatttcaa		180

ccacagtgaa ggctacatct cgagtcgaca agttttcaaa agcgatatca ttgtctctcc		240

gtccattctt t		251

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<210>     287
<211>     273
<212>     DNA
<213>     Glycine max

<400>     287

cttttgtgaa ggcctaggat tgctgagtca aacttgaatt gaagagtgaa gaaggagatg     60

gcagcaactt cttccttgtg ttcatcgacc ctccaatccc aaatcaatgg attctgcctt    120

cacaaaacct ctctttccca tcctcgttcc ctcactttct ccaggaagaa aatttcaacc    180

acagtgaagg ctacatctcg tgttgacaag ttttcaaaaa gcgatatcat tgtttctcca    240

tccattcttt ctgcaaactt tgcaaaattg ggg                                 273


<210>     288
<211>     273
<212>     DNA
<213>     Glycine max

<223>     unsure at all n locations
<400>     288

cacacacagt canactttng tgaaggccta ggattggtga gtcaaacttg aattgaaggt     60

gaagaaggag atggcagcaa cttcttcctt gtgttcatcg accctccaat cccaaatcaa    120

tggattctgc cttcacaaaa cctctctttc ccatcctcgt tccctcactt tctccaggaa    180

gaaaatttca accacagtga aggctacatc tcgtgttgac aagttttcaa aaagcggata    240

tcattgtttc tccatccatc tttctgcaaa ttt                                 273


<210>     289
<211>     259
<212>     DNA
<213>     Glycine max

<400>     289

cacagtcaca cttttgtgaa ggcctaggat tgctgagtca aacttgaatt gaaggtgaag     60

aaggagatgg cagcaacttc ttccttgtgt catcgaccc tccaatccca aatcaatgga    120

ttctgccttc acaaaacctc tctttcccat cctcgttccc tcactttctc caggaagaaa    180

atttcaacca cagtgaaggc tacatctcgt gttgacaagt tttcaaaaag cgatatcatt    240

gtttctccat ccattcttt                                                 259
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97

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<210>      290
<211>      246
<212>      DNA
<213>      Glycine max

<400>      290

tttcctcaag gcataggatt ggtgaggtaa acttgaattg aagtgaagaa ggagatggct    60

gcaacctctt ccttgtgctc atcgaccctc caatcccaga tcaatggatt cttgcttcac   120

aaaacctctc ttgctcatac tccttccctc actttctcca ggcggaaaat ttcaaccaca   180

gtgaaggcta catctcgagt cgacaagttt tcaaaaagcg atatcatgtg gtcgctccgt   240

ccattc                                                             246


<210>      291
<211>      262
<212>      DNA
<213>      Glycine max

<400>      291

gctggagttg tcttaaaccc cggtacccccc ttaagtgcaa tagaatatat ccttgatgtg    60

gttgatttgg tcttaattat gtccgtaaac cctggctttg gtggccagag ttttattgag   120

agtcaagtaa agaaaatttc tgatttgaga agattgtgtg cggagaaggg agtgaatcca   180

tggattgaag tagatggtgg agttggtcca gcaaatgcat acaaggtgat tgaggctgga   240

gccaatgcac tggttgctgg ct                                            262


<210>      292
<211>      282
<212>      DNA
<213>      Glycine max

<400>      292

agggtaccag atttttattaa ggcaggagct gatatagtca gtgttcattg tgaacaatct    60

tccaccatcc atttgcatcg tactgttaat caagtgaaaa gtctgggagc taaagctgga   120

gttgtcttaa accctgctac ccccttaagt gcaatagaat atgtcctgat gtggtggatt   180

tggtcttaat tatgtccgta aaccctggct ttggtggcca gagtttt att gagagtcaag   240

taaagaaaat ttctgacttg agaagagtgt gcgcggaaaa gg                      282
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98

<210> 293
<211> 249
<212> DNA
<213> Glycine max

<400> 293

gtcgctttgt tccaaatatt acaattggac ctcttgtggt tgatgcattg cgccctgtga   60

cagatcttcc tttggatgta cacctgatga ttgtagagcc tgaacaaagg gtaccagatt   120

ttattaaggc aggagctgat atagtcagtg ttcattgtga acaatcttcc accatccatt   180

tgcatcgtac agttaatcaa gtgaaaagtc tgggagctaa agctggagtt gtcttaaacc   240

ccggtaccc   249

<210> 294
<211> 264
<212> DNA
<213> Glycine max

<400> 294

ggtgaaagca gtagaattgg ctggttgtga ttggattcac gttgatgtaa tggatggtcg   60

ctttgttcca aatattacaa ttggacctct tgtggttgat gcattgcgcc ctgtgacaga   120

tcttcctttg gatgtacacc tgatgattgt agagcctgaa caaagggtac cagattttat   180

taaggcagga gctgatatag tcagtgttca ttgtgaacaa tcttccacca tccatttgca   240

tcgtacagtt aatcaagtga aaag   264

<210> 295
<211> 267
<212> DNA
<213> Glycine max

<223> unsure at all n locations
<400> 295

gtcagtgttc attgtgaaca atcttccncc atccatttgc atcctacagt taacncaagt   60

gaaaagtctg ggagctaaag ctggagttgt cttaaacccc ggtaccccct aagtgcaat   120

agaatatatc cttgatgtgg ttgatttggt cttaattatg tccgtaaacc ctggctttgg   180

tggccagagt tttattgaga gtcaagtaaa gaaaatttct gatttgagaa gattgtgtgc   240

99

ggagaaggga gtgaatccat ggattga   267

<210>   296
<211>   277
<212>   DNA
<213>   Glycine max

<223>   unsure at all n locations
<400>   296

gtccaattgt aatatttgga acaaaacggc catccattac aattngacct cttgtggttg   60

atgcattgcg ccctgtgaca nctcttcctt tggatgtaca cctgatgatt gtacagcctg   120

aacaaagggt accagatttt attaaggcag gagctgatat agtcagtgtt cattgtgaac   180

aatcttccac catccatttg catcgtactg ttaatcaagt gaaaagtctg ggagctaaag   240

ctggagttgt ctaaaccctg ctaccccctt aagtgca   277

<210>   297
<211>   263
<212>   DNA
<213>   Glycine max

<223>   unsure at all n locations
<400>   297

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ggttnatttg gtcttaattn tgtaccgtaa accctggctt tggtggccag agtttattg   120

agagtcaagt aaagaaattt ctgatttgag aagattgtgt gcggagaagg gagtgaatcc   180

atggattgaa gtagatggtg ggngttggtc cagcaaatgc atacaggtga tnggaggctg   240

gnagccaaac cntggtgcag gcc   263

<210>   298
<211>   388
<212>   DNA
<213>   Glycine max

<400>   298

ggagaaagaa agaaaagatg gaatgacac cgaaaatagc tccttcgatg ctctcttccg   60

acttcgccaa tttggcttcc gaggctcagc gcatgctcca cttcggcgcc gattggctcc   120

acatggacat catggatggg cattttgtcc ccaatttaac tattggcgct ccagttattg   180

100

aaagtttgag aaagcacaca aaggcatatt tggattgtca ccttatggtt acaaatcctc 240

ttgattatgt tgaacccttg gcaaaagctg gtgcttctgg ttttacattt cacgtagaga 300

catcaaaaga taactggaaa gaacttatcc aaagaatcaa gtcacatggc atgattcctg 360

gtgtagcatt aaagcctggg accccgt 388

<210>   299
<211>   368
<212>   DNA
<213>   Glycine max

<400>   299

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gtgacagatc ttcctttgga tgtacacctg atgattgtac agcctgaaca aagggtacca 120

gattttagta aggcacgagc tgatatagtc agtgttcatt gtgaacaatc ttccaccatc 180

catttgcatc gtactgttaa tcaagtgaaa agtctgggag ctaaagctgg agttgtctta 240

aaccctgcta ccccccttaag tgcaatagaa tatgtccttg atgtggtgga tttggtccta 300

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atttctga 368

<210>   300
<211>   350
<212>   DNA
<213>   Zea mays

<223>   unsure at all n locations
<400>   300

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tgctcttctt cgtgagaaga tggttgaggc agcatcggac aagtttattg ttattgttga 120

cgagacaaaa ctagttgatg ggttaggagg tagtggtcta gccatgccag tggaagttgt 180

gcagttctgc tggaagtaca accttgtaag attgcaggaa ctgtttaagg aggaaggagt 240

cgaggcaaag ctaaggtttg aaggcgacaa gccctatgtt actgacaact ncaactacat 300

cgtcgattta tacttcaaga cgccaatcaa ggatgcgttg gcagcaggac 350

<210>   301
<211>   264

101

<212>   DNA
<213>   Zea mays

<400>   301

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gttgaccctg acctcaacct tgtgaaaggg cggggtggtg ctcttcttcg tgagaagatg   120

gttgaggcag catcggacaa gtttattgtt attgttgacg agacaaaact agttgatggg   180

ttaggaggta gtggtctagc catgccagtg gaagttgtgc agttctgctg gaagtacaac   240

cttgtaagat tgcaggaact gttt   264

<210>   302
<211>   267
<212>   DNA
<213>   Zea mays

<400>   302

caaactgcgg ctgctgtaga tacgcgcgcc gtcactccaa ggtccaagcc tcccttgctc   60

ccgccaccgc ccctcaccat gggcagcgcc gccgcctctc cgcagccgtc tgggaatctg   120

acgcaggacg agctcaagcg cgtggcggcg caccgcgcgg tggagttcgt ggagcccggc   180

atgacgctgg gcctgggcac gggttccacg gccgcgcacg cgctggaccg tctgggctac   240

ctactccgcg tgggctcgct gtccggg   267

<210>   303
<211>   333
<212>   DNA
<213>   Zea mays

<400>   303

acgcccacgc gtccgtcccg ttcccgatcc tcatcacctc aaccccgcgc cgccccctcc   60

ccaccaccct cgccatggtc agcgccgccg cctcgccgcc gccgtccggg aagccgacgc   120

aggacgagct gaagcgcttg cggcgcacc gcgcggtgga gctcgtggag cccggcatga   180

cgctgggcct gggcacgggc tccacggcgg cgcacgcgct ggaccgcctg ggcgacctcc   240

tccgcgcggg cgcgctgccg ggggtggccg gcgtgccgac ctcgctcaag acggatgcgc   300

aagcggcgcg cgtcggcatc ccgctgctcc cgc   333

102

<210>   304
<211>   420
<212>   DNA
<213>   Zea mays

<400>   304

ggcgtgccca catccaagcg caccttcgag caggcgcagt cgctcggcat cccgctctgg   60

acgctcgacg acaacccgct catcgacctc gccatcgacg gtgccgacga ggttgaccct   120

gacctcaacc ttgtgaaagg gcggggtggt gctcttcttc gtgagaagat ggttgaggca   180

gcatcggaca agtttattgt tattgttgac gagacaaaac tagttgatgg gttaggaggt   240

agtggtctag ccatgccagt ggaagttgtg cagttctgct ggaagtacaa ccttgtaaga   300

ttgcaggaac tgtttaagga ggaaggagtc gaggcaaagc taaggtttga aggcgacaag   360

ccctatgtta ctgacaactc aaactacatc gtcgatttat acttcaagac gccaatcaag   420

<210>   305
<211>   432
<212>   DNA
<213>   Zea mays

<400>   305

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acaagtttat tgttattgtt gacgagacaa aactagttga tgggttagga ggtagtggtc   120

tagccatgcc agtggaagtt gtgcagttct gctggaagta caaccttgta agattgcagg   180

aactgtttaa ggaggaagga gtcgaggcaa agctaaggtt tgaaggcgac aagccctatg   240

ttactgacaa ctcaaactac atcgtcgatt tatacttcaa gacgccaatc aaggatgcgt   300

tggcagcagg acaggaaatt gcagctctgg aaggagttgt tgaccatggg ttgttcttga   360

acatggcgag ttcagtgatc attgctggaa cggacggtgt cagtgtcaaa acgaagtgag   420

tttttgagtt gc   432

<210>   306
<211>   461
<212>   DNA
<213>   Zea mays

<223>   unsure at all n locations
<400>   306

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gacaagttta ntgttattgt tgacgagaca aaactagttg atgggttagg aggtagtggt  120

ctagccatgc cagtggaagt tgtgcagttc tgctggaagt acaaccttgt aagattgcag  180

gaactgttta aggaggaagg agtcgaggca aagctaaggt ttgaaggcga caagccctat  240

gttactgaca actcaaacta catcgtcgat ttatacttca agacgccaat caaggatgcc  300

gttggcagca ggacaggaaa ttgcagctct ggaaggagtt gttgaccatg ggttgttctt  360

gaacatggcg agttcagtga tcattgctgg aacggacggt gtcagtgtca aaacgaaatg  420

agttttttgag ttgctttgtt ggttgngttg aaattttttt t                     461
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<210>   307
<211>   249
<212>   DNA
<213>   Glycine max

<400>   307

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ctcgatctcg ccatcgacgg cgccgacgag gtcgaccccg acctcaacct cgtcaaaggc   60

cgcggcggcg ccctcctccg cgagaagatg gtcgaggccg cctccgacaa gttcgtcgtg  120

gtcgtcgacg acaccaagct cgtggacggc ctcggcggaa gcgggctggc catgccggtg  180

gaggtggtcc agttctgctg gaagtacaat ctggatcggc ttcaggagct tttcaaggaa  240

gaaggtgtg                                                          249
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<210>   308
<211>   240
<212>   DNA
<213>   Glycine max

<400>   308

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gtcgaccccg acctcaacct cgtcaaaggc cgcggcggcg ccctcctccg cgagaagatg   60

gtcgaggccg cctccgacaa gttcgtcgtg gtcgtcgacg acaccaagct cgtggacggc  120

ctcgcggaag cgggctggcc atgccggtgg aggtggtcca gttctgctgg aagtacaatc  180

tggatcggct tcaggagctt ttcaaggaag aaggtgtgga agcaaaattg agattggagg  240
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<210>   309
<211>   262
<212>   DNA

104
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<213>   Glycine max

<400>   309

ggtcgacccc gacctcaacc tcgtcaaagg ccgcggcggc gccctcctcc gcgagaagat   60

ggtcgaggcc gcctccgaca agttcgtcgt ggtcgtcgac gacaccaagc tcgtggacgg   120

cctcggcgga agcgggctgg ccatgccggt ggaggtggtc cagatctgct ggaagtacaa   180

tctggatcgg cttcaggagc ttttcaagga agaaggtgtg gaagcaaaat tgagattgga   240

ggagagtggg aaccctacgt ca   262

<210>   310
<211>   263
<212>   DNA
<213>   Glycine max

<223>   unsure at all n locations
<400>   310

accacacatt caattttana cctctgggcg tggctagctt caacctttaa cattaacatg   60

gccattccct accccattt catcgccacc gagaaagccg ccatggacgc cggcctcctc   120

caccctcct ccccctccgt catcctcacc caagacgatt tgaagaaat cgccgcctac   180

aaggccgtcg agtacgtgga gtccggcatg atcctcggcc tcggcaccgg ctccaccgcc   240

aagcatgccg tcgaccgcat cgg   263

<210>   311
<211>   274
<212>   DNA
<213>   Glycine max

<400>   311

cttacattcc tttctccacc acacattcaa ttttgaacct ctgggactgg ctagcttcaa   60

cctttaacat taacatggcc attccctacc cccatttcat cgccaccgag aaagccgcca   120

tggacgccgg cctcctccac ccctcctccc cctccgtcat cctcacccaa gacgatttga   180

agaaaatcgc cgcctacaag gccgtcgagt acgtggagtc cggcatggtc ctcggcctag   240

gcaccggctc caccgccaag catgccgtcg accg   274

<210>   312
<211>   333

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<212>      DNA
<213>      Zea mays

<400>      312

ctcacctccc ctccactccc tttctcccct gactcctgct ctataggatc ctccgcctcc    60

atcgcctctc gcgcctccaa tcgccttcgg cgcttcgtcc gtcctgctcc acctcttctt   120

acgccggttg accctgacct caaccttgtg aaagggcggg gtggtgctct tcttcgtgag   180

aagatggttg aggcagcatc ggacaagttt attgttattg ttgacgagac aaaactagtt   240

gatgggttag gaggtagtgg tctagccatg ccagtggaag ttgtgcagtt ctgctggaag   300

tacaaccttg taagattgca ggactgttaa gga                               333


<210>      313
<211>      302
<212>      DNA
<213>      Zea mays

<400>      313

ggatggtgct cgggctcggg acgggctcca cggccgcctt cgccgtcgcc gagatcggcg    60

cgctcctggc cgcgggcaag ctcgagaaga tcgtcggcgt gcccacatcc aagcgcacct   120

tcgagcaggc gcagtcgctc ggcatcccgc tctccacgct cgacgacaac ccgctcatcg   180

acctcgccat cgacggtgcc gacgaggttg accctgacct caaccttgtg aaagggcggg   240

gtggtgctct tcttcgtgag aagatggttg aggcagcatc ggacaagttt attgttattg   300

tt                                                                  302


<210>      314
<211>      244
<212>      DNA
<213>      Glycine max

<400>      314

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gggatccccc tctccgatct cgacgcccac cccgccatcg atctcgccat cgacggcgcc   120

gacgaggtcg atcccttcct caacctcgtc aagggccgtg cggctccct cctccgagaa   180

aaaatggtcg aaggcgcatg caagaagttc atcgtcatcg ttgatgagtc caagctcgta   240

aact                                                                244
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106

<210> 315
<211> 267
<212> DNA
<213> Glycine max

<400> 315

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agggccgtgg cggctccctc ctccgagaaa aaatggtcga aggcgcatgc aagaagttca   120

tcgtcatcgt tgatgagtcc aagctcgtaa actatttggg gggtagtggg ttggccatgc   180

ccgttgaggt tattaagttc tgttggaggt tcaccgcggc gaggttgcag aagcttcttg   240

aggaggctgg gtgcgttgcc aggctca   267

<210> 316
<211> 291
<212> DNA
<213> Glycine max

<223> unsure at all n locations
<400> 316

gatttgaaga aaatcgcngc ctacaaggcc gtcgagtacg tggagtccgg catggtcctc   60

ggcctaggca ccggctccan cgccaagcat gccgtcganc gcatcggcga gctcctccgc   120

cagggcaagc tcaaggacat cgtcggaatc cccacctcca caaaaaccca cgaacaagcc   180

ctctccctcg ggatccccct ctccgatctc gacgcccacc cgccatcga tctcgccatc   240

gacggcgccg acgaggtcga ccccttcctc aacctcgtca agggccgtgg g   291

<210> 317
<211> 265
<212> DNA
<213> Glycine max

<400> 317

agacgacctc aagaaaatcg ccgcctacaa ggccgtcgag tacgtcgagt ccggcatggt   60

cctcggcctc ggcaccggct ccactgccaa gcacgccgtc gaccgcatcg gcgagctcct   120

ccgccaagga aaactcaaag acatcgtcgg catccccacc tccaccaaaa cccacgacca   180

ggccctctcc ctcggcatcc ccctctccga tctcgactcc caccccaccg tcgatctcgc   240

107

catcgacggc gccgacgagg tcgat   265

<210>   318
<211>   265
<212>   DNA
<213>   Glycine max

<223>   unsure at all n locations
<400>   318

cacaccacna cgcctccacg ngccttattc nanncacccc taantngngt aaacngcgca   60

ctaccacncc actaccctcc ccgccatcng cgccatcacc ctcacccagg acgaccncaa   120

gagactcgcc gccgacaagg ccgtggagtc cgtcaagagc ggcatggtcc tcggcctagg   180

caccggctcc actgctgcct tcgtcgtcgc caagcttggc gcccttctcg cctccggcca   240

actctccgac atcgtcggtg tcccc   265

<210>   319
<211>   320
<212>   DNA
<213>   Zea mays

<400>   319

gagaagtcgg tcaacacgat ccggttcctg gccatcgacg ccgtcgagaa ggccaactcc   60

ggccacccgg gcctccccat gggctgcgcg cccatgggcc acgtcctcta cgacgaggtc   120

atgcgctaca accccaagaa cccctactgg ttcaaccgcg accgcttcgt cctctccgcc   180

ggccacggct gcatgctcca gtacgccctc ctccacctcg ccggttacga cagcgttaag   240

gaggaggact tgaagcagtt ctggcaatgg ggaagcagaa caccgggcca ccctgagaac   300

tttgagactc caggagttga   320

<210>   320
<211>   235
<212>   DNA
<213>   Zea mays

<400>   320

gtacaccatc tctgacaact ctaccggcaa caagccgggc atcattgtga tgggcaccgt   60

ctccgagctg tagatcgcgg ccaaggccgt cgacgagctg aggaaggagg ggaagacggt   120

ccgcgtcgtc tcgttcgtct cctgggaact ctttgatgag cagtcggatg agcacaagga   180

108

gatcgtcctc cctgccgccg tcacagcgag gatcagcatc gaagccgggt ccact   235

<210>   321
<211>   276
<212>   DNA
<213>   Zea mays

<400>   321

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aacgttgcac aataaggtat cagaccaggg ctgtgaacag cgatgccatt cgaaatggca   120

cccatagcat gctctcgcac accgaagcga atgtttctct cttcaggagt atccctctgg   180

atttctccaa acttcttaag cagtgtcatg tttgacgttg cgagatccga actacctcca   240

agaaatccag gtattacttt ggcaagtgca ttcaag   276

<210>   322
<211>   292
<212>   DNA
<213>   Zea mays

<400>   322

gcaaccaggc agaaccttgg atggccctat gacacattct ttgtaccaga ggacgtcaag   60

agtcactgga gccgccacac acccgaaggt gctgcacttg aggctgattg gaacgctatg   120

tttgcagagt acgagaagaa gtatgcagat gatgcagcaa ccttgaaaag tatcatcacg   180

ggggagttac ccactggctg ggttgatgct cttcctaaat acactccaga gagcccagga   240

gatgccacca ggaacctctc ccagcagtgc ctgaacgcgc ttgctaatgt tg   292

<210>   323
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<212>   DNA
<213>   Zea mays

<400>   323

tggaagtgca ctgggtgcca aagaggttga agcaaccagg cagaaccttg gatggcccta   60

cgacacattc tttgtaccag aggacgtcaa gagtcactgg agccgccaca cacccgaagg   120

tgctgcactt gaggctgatt ggaacgctaa gtttgcagag tacgagaaga agtatgcaga   180

tgatgcagca accttgaaaa gtatcatcac ggggggagtta cccactggct gggttgatgc   240

109

tcttcctaaa tacactccag agagcccagg agatgccacc taggaactct cccag   295

<210>   324
<211>   285
<212>   DNA
<213>   Zea mays

<400>   324

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gttacccact ggctgggttg atgctcttcc taaatacact ccagagagcc caggagatgc   120

caccaggaac ctctcccagc agtgcctgaa cgcccttgct aatgttgtgc ctggtcttat   180

cggaggcagt gctgatcttg catcctccaa catgactctg ctgaagatgt ttggtgactt   240

ccagaaggat acagctgaag agcgcaatgt ccgcttcgga gtcag   285

<210>   325
<211>   296
<212>   DNA
<213>   Zea mays

<400>   325

ggccacagtc aaggagccgg acacaccgaa gcggagcacc tgaggccgat tggaacgcta   60

tgtttgcaga gtacgagaag aagtatgcag atgatgcagc aaccttgaaa agtatcatca   120

cggggggagtt acccactggc tgggttgatg ctcttcctaa atacactcca gagagcccag   180

gagatgccac caggaacctc tcccagcagt gcctgaacgc gcttgctaat gttgtgcctg   240

gtcttattgg aggcagtgct gatcttgcat cctccaacat gactctgctg aagatg   296

<210>   326
<211>   293
<212>   DNA
<213>   Zea mays

<400>   326

caggagatgc caccaggaac ctctcccagc agtgcctgaa cgcgcttgct aatgttgtgc   60

ctggtcttat tggaggcagt gctgatcttg catcctccaa catgactctg ctgaagatgt   120

ttggtgactt ccagaaggat acagctgaag agcgcaatgt ccgctttgga gtcagagagc   180

acggaatggg cgccatttgc acaggcattg ctctgcacag cccagggttt gttccgtact   240

110

gtgctacagt ctttgtcttc actgtttaca tgagaggtgc catgaggatc tcg   293

<210>   327
<211>   271
<212>   DNA
<213>   Zea mays

<400>   327

gtcaagagtc actggagccg ccacacaccc gaaggtgctg cacttgaggc tgattggaac   60

gctatgtttg cagagtacga gaagaagtat gcagatgatg cagcaacctt gaaaagtatc   120

atcacggggg agttacccac tggctgggtt gatgctcttc ctaaatacac tccagagagc   180

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cctggtctta ttggaggcag tgctgatctt g   271

<210>   328
<211>   285
<212>   DNA
<213>   Zea mays

<400>   328

ccaccaggac cctctcccag cagtgcctga acgcgcttgc taatgttgtg cctggtctta   60

ttggaggcag tgctgatctt gcatcctcca acatgactct gctgaagatg tttggagact   120

tccagaagga tacagctgaa gagcgcaatg tccgctttgg agtcagagag cacggaatgg   180

gcgccatttg caacggcatt gctctgcaca gcccagggtt tgttccgtac tgtgctacat   240

tctttgtctt cactgattac atgagaggtg ccatgaggat ctcgg   285

<210>   329
<211>   274
<212>   DNA
<213>   Zea mays

<400>   329

ctcgagcgaa tcggctcgag atcacggggg agttacccac tgcctgggtt gatgctcacc   60

ctaaatacac tccagagagc ccaggagatg ccaccaggaa cctctcccag cagtgcctga   120

acgcccttgc taatgttgtg cctggtctta tcggaggcag tgctgatctt gcatcctcca   180

acatgactct gctgaagatg tttggtgact tccagaagga tacagctgaa gagcgcaatg   240

111

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tccgcttcgg agtcagagag cacggaatgg gcgc                                    274


<210>       330
<211>       187
<212>       DNA
<213>       Zea mays

<400>       330

ccactggctg ggttgatgct cttcctaaat acactccaga gagcccagga gatgccacca    60

ggaacctctc ccagcagtgc ctgaacgccc ttgctaatgt tgtgcctggt cttatcggag   120

gcagtgctga tcttgcatcc tccaacatga ctctgctgaa gatgtttggt gacttccaga   180

aggatac                                                              187


<210>       331
<211>       219
<212>       DNA
<213>       Zea mays

<400>       331

gaagtatgca gatgatgcag caaccttgaa aagtatcatc acgggggagt tacccactgg    60

ctgggttgat gctcttccta aatacactcc agagagccca ggagatgcca ccaggaacct   120

ctcccagcag tgcctgaacg cgcttgctaa tgttgtgcct ggtcttattg gaggcagtgc   180

tgatcttgca tcttccaaca tgactctgct gaagatgtt                           219


<210>       332
<211>       177
<212>       DNA
<213>       Zea mays

<400>       332

tcttattgga ggcagtgctg atcttgcatc ctccaacatg actctgctga agatgtgggg    60

tgactcccag aaggatacac tgaagagcgc aatgtccgct ttggagtcag agagcacgga   120

atgggcgcca tttgcaacgg cattgctctg cacagcccag ggtttgttcc gtactgt      177


<210>       333
<211>       261
<212>       DNA
<213>       Zea mays
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112

<400>　　　　333

cgctcgagcg catcggctcg agatcacggg ggagttaccc actggctggg ttgatgctat　60

tcctaaatac actccagaga gcccaggagc tgccacagga ccctctccca gcagtgcctg　120

aacgcccttg ctaatgttgt gcctggtctt atcggaggca gtgctgatct tgcatcctcc　180

aacatgactc tgctgaagat gtttggtgac ttccagaagg atacagctga agagcgccat　240

gtccgcttcg gagtcagaga g　261

<210>　　　　334
<211>　　　　203
<212>　　　　DNA
<213>　　　　Zea mays

<400>　　　　334

caggggtctt ggcaagctga tagctttcta cgatgacaac cacatttcca tcgacggaga　60

cacggagatt gcattcacag aggacgtgag cacccgcttc gaggctcttg ggtggcacac　120

gatctgggtt aagaatggga acaccggata tgatgacatc cgcgcaccat taaggaggcg　180

aaggcagtca ctgacaagcc cac　203

<210>　　　　335
<211>　　　　289
<212>　　　　DNA
<213>　　　　Zea mays

<400>　　　　335

gagcgcaatg tccgcttcgg agtcagagag cacggaatgg gcgccatttg caacggcatt　60

gctctgcaca gcccagggtt tgttccgtac tgtgctacat tctttgtctt cactgattac　120

atgagaggtg ccatgaggat ctcggccctg tctgaagccg gagtcatcta tgtcatgacc　180

cacgactcta ttggtctcgg agaagatggc ccgacccatc agcccatcga gcacctggtg　240

agcttccgtg cgatgccgaa catactgatg ctccgccctg ctgatggca　289

<210>　　　　336
<211>　　　　305
<212>　　　　DNA
<213>　　　　Zea mays

<400>　　　　336

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gatgtttggt gacttccaga aggatacagc tgaagagcgc aatgtccgct tcggagtcag    60

agagcacgga atgggcgcca tttgcaacgg cattgctctg cacagcccag ggtttgttcc   120

gtactgtgct acattctttg tcttcactga ttacatgaga ggtgccatga ggatctcggc   180

cctgtctgaa gccggagtca tctatgtcat gacccacgac tctattggtc tcggagaaga   240

tggcccgacc catcagccca tcgagcacct ggtgagcttc cgtgcgatgc cgaacatact   300

gatgc                                                               305


<210>      337
<211>      275
<212>      DNA
<213>      Zea mays

<400>      337

attacatgag aggtgccatg aggatctcgg ccctgtctga agccggagtc atctatgtca    60

tgacccacga ctctattggt ctcggagaag atggcccgac ccatcagccc atcgagcacc   120

tggtgagctt ccgtgcgatg ccgaacatac tgatgctccg ccctgctgat ggcaacgaga   180

ctgccggagc atacaaagtc gcggtcctca acaggaagag gccgtccatc ctcgctctct   240

ccaggcaaaa gctccctcac ctgcctggca cctcg                              275


<210>      338
<211>      288
<212>      DNA
<213>      Zea mays

<400>      338

agcacctggt gagcttccgt gcgatgccga acatactgat gctccgccct gctgatggca    60

acgagactgc cggagcatac aaagtcgcgg tcctcaacag gaagaggccg tccatcctcg   120

ctctctccag gcaaaagctc cctcacctgc ctggcacctc gatcgagggc gtggagaagg   180

gcgggtacac catctctgac aactcgaccg gcaacaagcc tgacatcatt gtgatgggca   240

ccggctccga gctggagatc gcggccaagg ccgccgacga gctgagga                288


<210>      339
<211>      280
<212>      DNA
<213>      Zea mays
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114

<400> 339

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ctgccggagc atacaaagtc gcggtcctca acaggaagag gccgtccatc ctcgctctct    60

ccaggcaaaa gctccctcac ctgcctggca cctcgatcga gggcgtggag aagggcgggt   120

acaccatctc tgacaactcg accggcaaca agcctgacat cattgtgatg ggcaccggct   180

ccgagctgga gatcgcggcc aaggccgccg acgagctgag gaaggagggg aagacggtcc   240

gcgtcgtctc gttcgtctcc tgggaactct ttgatgagca                         280
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<210>   340
<211>   255
<212>   DNA
<213>   Zea mays

<400>   340

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gtctcggaga agatggcccg acccatcagc ccatcgagca cctggtgagc ttccgtgcga    60

tgccgaacat actgatgctc cgccctgctg atggcaacga gactgccgga gcatacaaag   120

tcgcggtcct caacaggaag aggccgtcca tcctcgctct ctccaggcaa aagctccctc   180

acctgcctgg cacctcgatc gagggcgtgg agaagggcgg gtacaccatc tctgacactc   240

gaccggcaac aagcc                                                     255
```

<210>   341
<211>   254
<212>   DNA
<213>   Zea mays

<400>   341

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catctatgtc atgacccacg actctattgg tctcggagaa gatggcccga cccatcagcc    60

catcgagcac ctggtgagct tccgtgcgat gccgaacata ctgatgctcc gccctgctga   120

tggcaacgag actgccggag catacaaagt cgcggtcctc aacaggaaga ggccgtccat   180

cctcgctctc tccaggcaaa agctccctca cctgcctggc acctcgatcg agggcgtgga   240

gaagggcggg taca                                                      254
```

<210>   342
<211>   273
<212>   DNA
<213>   Zea mays
```

115

<400>        342

ggagatcgcg gccaaggccg ccgacgagct gaggaaggag gggaagacgg tccgcgtcgt    60

ctcgttcgtc tcctgggaac tctttgatga gcagtcggat gagtacaagg agagcgtcct   120

ccctgccgcc gtcacagcga ggatcagcat cgaggccggg tccactctcg gctggcagaa   180

gtacgtcgga gcccagggca aggccattgg catcgacaag ttcggcgcga gtgctcctgc   240

cgggacgatc tacaaggagt acggcatcac cgt                                273


<210>        343
<211>        301
<212>        DNA
<213>        Zea mays

<400>        343

ctatgtcatg acccacgact ctattggtct cggagaggat ggcccgaccc atcagcccat    60

cgagcacctg gtgagcttcc gtgcgatgcc gaacatactg atgctccgcc ctgctgatgg   120

caacgagact gccggagcat acaaagtcgc ggtcctcaac aggaagaggc cgtccatcct   180

cgctctctcc aggcaaaagc tccctcacct gcctggcacc tcgatcgacg gcgtggagaa   240

tggcgggtac accatctctg acaactcgac cggcaacaag cctgacctca ttgtgatggg   300

c                                                                   301


<210>        344
<211>        276
<212>        DNA
<213>        Zea mays

<400>        344

gcctgacatc attgtgatgg gcaccggctc cgagctggag atcgcggcca aggccgccga    60

cgagctgagg tcatgagggg aagacggtcc gcgtcgtctc gttcgtctcc tgggaactct   120

ttgatgagca gtcggatgag tacaaggaga gcgtcctccc tgccgccgtc acagcgagga   180

tcagcatcga ggccgggtcc actctcggct ggcagaagta cgtcggagcc cagggcaagg   240

ccattggcat cgacaagttc ggcgcgagtg ctcctg                             276


<210>        345
<211>        300


116

<212>　　　　DNA
<213>　　　　Zea mays

<400>　　　　345

cgacgagctg aggaaggagg ggaagacggt ccgcgtcgtc tcgttcgtct cctgggaact　60

ctttgatgag cagtcggatg agtacaagga gagcgtcctc cctgccgccg tcacagcgag　120

gatcagcatc gaggccgggt ccactctcgg ctggcagaag tacgtcggag cccagggcaa　180

ggccattggc atcgacaagt tcggcgcgag tgctcctgcc gggacgatct acaaggagta　240

cggcatcacc gtggagagca tcattgcagc tgccaagagc ttttaagagc taacaacggt　300


<210>　　　　346
<211>　　　　316
<212>　　　　DNA
<213>　　　　Zea mays

<400>　　　　346

ggtgccatga ggatctcggc cctgtctgaa gccggagtca tctatgtcat gacccacgac　60

tctattggtc tcggagagga tggcccgacc catcagccca tcgagcacct ggtgagcttc　120

cgtgcgatgc cgaacatact gatgctccgc cctgctgatg caacgagac tgccggagca　180

tacatcgccg cggtcctcaa caggaagagg ccgtccatcc tcgctctctc caggcaaaag　240

ctccctcacc tgcctggcac ctcgatcgag ggcgtggaga agggcgggta caccatctct　300

gacaactcga ccggca　316


<210>　　　　347
<211>　　　　299
<212>　　　　DNA
<213>　　　　Zea mays

<400>　　　　347

ctttgatgag cagtcggatg agtacaagga gagcgtcctc cctgctgccg tcacagcgag　60

gatcagcatc gaggccgggt ccactcttgg ctggcagaag tacgtcggag cccagggcaa　120

ggccattggc atcgacaagt tcggcgcgag tgctcctgcc gggacgatct acaaggagta　180

cggcatcacc gtggagagca tcattgcagc tgccaagagc ttttaagagc taacaacggt　240

ctggagtttt ttttattgtc gtcgttgatg ccaaaggaac actgtacctt gaggacagt　299


117

<210> 348
<211> 242
<212> DNA
<213> Zea mays

<400> 348

caggcgtcct ccctgctgcc gtcacagcga ggatcagcat cgaggccggg tccactcttg    60

gctggcagaa gtacgtcgga gcccagggca aggccattgg catcgacaag ttcggcgcga   120

gtgctcctgc cgggacgatc tacaaggagt acggcatcac cgtggagagc atcattgcag   180

ctgccaagag cttttaagag ctaacaacgg tctggagttt tttttattgt cgtcgttgat   240

gc                                                                  242


<210> 349
<211> 287
<212> DNA
<213> Zea mays

<400> 349

tctcgagccg gtcctcaaca ggaagaggcc gtccatcctc gctctctcca ggcaaaagct    60

ccctcacctg cctggcacct cgatcgaggg cgtggagaag ggcgggtaca ccatctctga   120

caactcgacc ggcaacaagc ctgacatcat tgtgatgggc accggctccg agctggagat   180

cgcggccaag gccgccgacg agctgaggaa ggaggggaag acggtccgcg tcgtctcgtt   240

cgtctcctgg gaactctttg atgagcagtc ggatgagtac aaggaga              287


<210> 350
<211> 265
<212> DNA
<213> Zea mays

<400> 350

gtccactctc ggctggcaga agtacgtcgg agcccagggc aaggccattg gcatcgacaa    60

gttcggcgcg agtgctcctg ccgggacgat ctacaaggag tacggcatca ccgtggagag   120

catcattgca gctgccaaga gcctttaaga gctaacaacg gtctggagtt tttcttattg   180

tcgtcgttga tgccaaagga acactgtacc tagaggacat cctatgcctc ggagcttgga   240

ataatgatga tggagggagc ggaag                                         265


118

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<210>      351
<211>      336
<212>      DNA
<213>      Zea mays

<400>      351

cttcgaggct cttgggtggc acacgatctg ggttaagaat gggaacaccg gatatgatga   60

catccgcgca ccattaagga ggcgaaggca gttactgaca agcccacctt gatcaaggtg  120

actaccacga tcggttttgg atctcccaac aaggccaact catacagtgt tcatggaagt  180

gcactgggtg ccaaataggt tgaagcaacc aggcagaacc ttggatggcc ctatgacaca  240

ttctttgtac cagaggacgt caagagtcac tggagccgcc acacacccga aggtgctgca  300

cttgaggctg attggaacgc taagtttgca gagtac                             336


<210>      352
<211>      275
<212>      DNA
<213>      Zea mays

<400>      352

tgatcacccg cttcgaggct cttgggtggc acactatctg ggttaagaat gggaacaccg   60

gatatgatga catccgcaca ccattaagga ggcgaaggca gttactgaca agcccacctt  120

gatcaaggtg actaccacat cggttttgga tctcccaaca aggccaactc atacagtgtt  180

tatggaagtg cactgggtgc caaagaggtt gaagcaacca ggcagaacct tggatggccc  240

tatgacacat tctctgtacc agaggacgtc aagag                             275


<210>      353
<211>      286
<212>      DNA
<213>      Zea mays

<400>      353

ccggatatga tgacatccgc gcaccattaa ggaggcgaag gcagttactg acaagcccac   60

cttgatcaag gtgactacca cgatcggttt tggatctccc aacaaggcca actcatacag  120

tgttcatgga agtgcactgg gtgccaaaga ggttgaagca accaggcaga accttggatg  180

gccctatgac acattctttg taccagagga cgtcaagagt cactggagcc gccacacacc  240

cgaacgtgct gcacttgagg ctgattggaa cgctaagttt gcagag                 286
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119

```
<210>      354
<211>      249
<212>      DNA
<213>      Zea mays

<400>      354

cttgggtggc acacgatctg ggttaagaat gggaacaccg gatatgatga catccgcgca      60

ccattaagga ggcgaaggca gttactgaca agcccacctt gatcaaggtg actaccacga     120

tcggttttgg atctcccaac aaggccaact catacagtgt tcatggaagt gcactgggtg     180

ccaaagaggt tgaagcaacc aggcagaacc ttggatggcc ctatgacaca ttctttgtac     240

cagaggacg                                                            249


<210>      355
<211>      423
<212>      DNA
<213>      Zea mays

<400>      355

agctccctca cctgcctggc acctcgatcg agggcgtgga gaagggcggg tacaccatgt      60

ctgacaactc gaccggcaac aagcctgacc tcattgtgat gggcaccggc tccgagctgg     120

agatcgcggc caaggccgcc gacgagctga ggaaggaggg caagacggtc cgcgtcgtct     180

cgttcgtctc ctgggaactc tttgatgagc agtcggatga gtacaaggag agcgtcctcc     240

ctgctgccgt cacagcgagg atcagcatcg aggccgggtc cactcttggc tggcagaagt     300

acgtcggagc ccagggcaag gccattggca tcgacaagtt cggcgcgagt gctcctgccg     360

ggacgatcta caaggagtac ggcatcaccg tggagagcat cattgcagct gccaagaagc     420

ttt                                                                  423


<210>      356
<211>      385
<212>      DNA
<213>      Zea mays

<400>      356

caaccggcac caagcctgac atcattgggt tgggcaccgg ctccgagctg gagatcgcgg      60

gcaatgcggc cgacgagctg aggaaggagg ggaagacggt ccgcgtcgtc tcgttcgtct     120
```

120

cctgggaact ctttgatgag cagtcggatg agtacaagga gagcgtcctc cctgccgacg 180

tcacagcgag gatcagcatc gaggccgggt ccactctcgg ctggcagaag tacgtcggag 240

cccaaggcaa ggccattggc atcgacaagt tcggcgcgag tgctcctgcc gggacgatct 300

acaaggagta cggcatcacc gtggagagca tcattgcaac tgccaagagc ttttaagagc 360

taacaacggt ctgggagttt ttttt   385

<210>   357
<211>   279
<212>   DNA
<213>   Glycine max

<400>   357

atgctaagtt tgctgagtat gaaaagaaat acaaggagga agctgcagaa ttgaaatcta 60

ttatcaatgg tgaattccct gctggttggg agaaagcact tccgacatac actccagaga 120

gcccagcgga tgccaccaga aacctgtctc aaacaaacct taatgccctt gcaaaggttc 180

ttcccggtct gcttggtggc agtgcagatc ttgcttcttc caacatgacc ttgctcaaaa 240

tgttcgggga cttccagaag gatactccag cagagcgta   279

<210>   358
<211>   246
<212>   DNA
<213>   Glycine max

<400>   358

ccttgctcaa aatgttcggg gacttccaaa aggatactcc agcagagcgt aatgttagat 60

tcggtgttag agaacacgga atgggagcta tctgcaacgg cattgctctt cacagccctg 120

gactgattcc atattgtgca accttctttg tattcactga ctacatgaga ggtgccataa 180

ggctttctgc gctgtctgag ctggggtta tttatgtcat gacccatgat tcaataggac 240

ttggag   246

<210>   359
<211>   220
<212>   DNA
<213>   Glycine max

<400>   359

121

caataaccag tgagagtcac aatcaaatag tagggaatgg gttaatcctt ggaacagggc   60

tgattccata ttgtgcaacc ttctttgtat tcactgacta catgagaggt gccataaggc   120

tttctgcgct gtctgaggct ggggttattt atgtcatgac ccatgattca ataggacttg   180

gagaagatgg gccaacccac cagcctattg agcacctagc   220

<210>   360
<211>   263
<212>   DNA
<213>   Glycine max

<400>   360

cagaaacctg tctcaaacaa accttaatgc ccttgcaaag gttcttcccg tctgcttgg   60

tggcagtgca gatcttgctt cttccaacat gaccttgctc aaaatgttcg gggacttcca   120

aaaggatact ccagcagagc gtaatgttag attcggtgtt agagaacacg gaatgggagc   180

tatctgcaat ggcattgctc ttcacagccc tggactgatt ccatattgtg caaccttctt   240

tgtattcact gactacatga gag   263

<210>   361
<211>   308
<212>   DNA
<213>   Glycine max

<400>   361

tccttcccat cattctctgg cctcaagtca cattctacat gcaaagcagc agcagccacg   60

tcctcgcgta gaaggggtgc ttgtccatcc accaacgttg ttcgagccgc tgcggttgag   120

acactcgacc aaaccaccga ggtttctctg gtggagaaat ccgtcaacac cattcggttt   180

ttggccattg atgcagttga gaaggccaac tctggtcacc ctggtctccc catggggtgt   240

gctccaatgg gtcacattct ctacgatgag ataatgaggt acaatcctaa gaaccccgtt   300

ggttcaac   308

<210>   362
<211>   263
<212>   DNA
<213>   Glycine max

<400>   362

122

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tgctgtttca gccagagtta gcattgaggc aggatcaaca tttgggtggg agaaaattgt   60

tggagcaaaa gggaaaagca ataggcattg atcgtttttgg agctagtgct ccagctggaa  120

gaatatacaa agaatttggt atcactaagg aagctgttgt tgctgcagct aaagagctta  180

tctagaactt ttgatttttt ttgccttctg gttttggttg agagcattcc atgtcatgaa  240

taagaaaaag gttaaatatc ctt                                          263
```

<210>   363
<211>   332
<212>   DNA
<213>   Glycine max

<223>   unsure at all n locations
<400>   363

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aaccattggt tatggttctc ctaacaaggc taactcctac agtgtgcatg gaagtgcact   60

gggtgccaaa gaagttgang ccacaaggca gaaccttgga tggtcacatg agccattcca  120

cgtgcctgag gatgtcaaaa agcattggag tcgccacacc cctgagggtg ctgcacttga  180

agctgaatgg aatgctaagt ttgctgagta tgaaaagaat acaaggagga agctgcagaa  240

ttgaaatcta ttatcaatgg tgaattccct gctggttggg agaaagcact tccgacatac  300

actccagaga gcccacgggt gccaccagaa ac                                332
```

<210>   364
<211>   247
<212>   DNA
<213>   Glycine max

<400>   364

```
aaccattggt tatggttctc ctaacaaggc taactcctac agtgtgcatg gaagtgcact   60

gggtgccaaa gaagttgatg ccacaaggca gaaccttgga tggtcacatg agccattcca  120

cgtgcctgag gatgtcaaaa agcattggag tcgccacacc cctgagggtg ctgcacttga  180

agctgaatgg aatgctaagt ttgctgagta tgaaaagaaa tacaaggagg aagctgcaga  240

attgaaa                                                           247
```

<210>   365
<211>   238
<212>   DNA

123
```

<213>   Glycine max

<400>   365

caaggctaac tcctacagtg tgcatggaag tgcactgggt gccaaagaag ttgatgccac   60

aaggcagaac cttggatggt cacatgagcc attccacgtg cctgaggatg tcaaaaagca   120

ttggagtcgc cacacccctg agggtgctgc acttgaagct gaatggaatg ctaagtttgc   180

tgagtatgaa aagaaataca aggaggaagc tgcagaattg aaatctatta tcaatggt   238

<210>   366
<211>   253
<212>   DNA
<213>   Glycine max

<400>   366

gggtgccaaa gaagttgatg ccacaaggca gaaccttgga tggtcacatg agccattcca   60

cgtgcctgag gatgtcaaaa agcattggag tcgccacacc cctgagggtg ctgcacttga   120

agctgagtgg aatgctaagt ttgctgagta tgaaaagaaa tacaaggagg aagctgcaga   180

attgaaatct attatcaatg gtgaattccc tgctggttgg gagaaagcac ttccgacata   240

cactccagag agc   253

<210>   367
<211>   171
<212>   DNA
<213>   Glycine max

<400>   367

gttctcctaa caaggctaac tcctacagtg tgcatggaag tgcactgggt gccaaagaag   60

ttgatgccac aaggcagaac cttggatggt cacatgagcc attccacgtg cctgaggatg   120

tcaaaaagca ttggagtcgc cacacccctg agggtgctgc acttgaagct g   171

<210>   368
<211>   277
<212>   DNA
<213>   Glycine max

<400>   368

atacgagcct ttccatgtgc cagaagatgt taaaaagcat tggagtcgcc atacccctga   60

124

gggtgctaaa cttgaagctg agtggaatgc caagtttgca gaatatgaga agaaatacag   120

tgaggaagct gcagagctga aggctattat tactgtgaat taccagctgg ttgggagaaa   180

gcacttccga catacactcc agaaagccct gctgatgcta caagaaatct gtctcagcaa   240

aatctaaatg cccttgttaa ggttcttcct ggtctac   277

<210>   369
<211>   268
<212>   DNA
<213>   Glycine max

<400>   369

gctacaagga agaatcttgg atggccatac gagcctttcc atgtgccaga agatgtcaag   60

aagcattgga gtcgccatac acctgagggt gctaaacttg aagctgagtg gaatgccaag   120

tttgtggaat atgagaagca atacagtgag gaagctgcag agctgaaggc tattattact   180

ggcgaattac cagcaagttg ggagaaagca cttccgacat acacaccaga aagccctgct   240

gatgctacaa gaaatctgtc tcagcaaa   268

<210>   370
<211>   258
<212>   DNA
<213>   Glycine max

<400>   370

taaagaagca aaggctgtca agacaaacc cactttgatc aaggtaacca ctaccattgg   60

atttggttct ccaaacaagg ctaattccta cagtgttcat gggagtgcat taggtgctaa   120

agaagtggat gctacaagga agaatcttgg atggccatac gagcctttcc atgtgccaga   180

agatgtcaag aagcattgga gtcgccatac acctgagggt gctaaacttg aagctgagtg   240

gaatgccaag tttgtgga   258

<210>   371
<211>   247
<212>   DNA
<213>   Glycine max

<400>   371

gccatacccc tgagggtgct aaacttgaag ctgagtggaa tgccaagttt gcagaatatg   60

125

agaagaaata cagtgaggaa gctgcagagc tgaaggctat tattactggt gaattaccag 120

ctggttggga gaaagcactt ccgacataca ctccagaaag ccctgctgat gctacaagaa 180

atctgtctca gcaaaatcta aatgcccttg ttaaggttct tcctggtcta cttggtggca 240

gtgcaga 247

<210> 372
<211> 264
<212> DNA
<213> Glycine max

<223> unsure at all n locations
<400> 372

ggagtcgcca tacacctgag ggtgctaaac ttgaagctga gtggtntgcc aagtttgtgg 60

aatatgagaa gcaatacagt gaggaagctg cagagctgaa ggctattatt actggcgaat 120

taccagctgg ttgggagaaa cacttccgac atacacacca gaaagccctg ctgatgctac 180

aagaaatctg tctcagcaaa atctaaatgc ccttgttaag gttcttcctg gtctacttgg 240

tggtagtgca gatcttgcct cttc 264

<210> 373
<211> 245
<212> DNA
<213> Glycine max

<400> 373

gtggaatgcg aagtttgcag aatatgagaa gacatacagt gaggaagctg cagagctgaa 60

ggctattatt actggtgaat taccagctgg ttgggagaaa gcacttccga catacactcc 120

agaaagccct gctgatgcta caagaaatct gtctcagcaa atctaaatg cccttgttaa 180

ggttcttcct ggtctacttg gtggcagtgc agatcttgcc tcttccaaca tgaccttgtt 240

gaaat 245

<210> 374
<211> 242
<212> DNA
<213> Glycine max

<400> 374

tggaatgcca agtttgcaga atatgagaag aaatacagtg aggaagctgc agagctgaag 60

126

gctattatta ctggtgaatt accagctggt tgggagaaag cacttccgac atacactcca   120

gaaagccctg ctgatgctac aagaaatctg tctcagcaaa atctaaatgc ccttgttaag   180

gttcttcctg gtctacttgg tggcagtgca gatcttgcct cttccaacat gaccttgttg   240

aa   242

<210>   375
<211>   246
<212>   DNA
<213>   Glycine max

<400>   375

gcagaatatg agaagaaata cagtgaggaa gctgcagagc tgaaggctat tattactggt   60

gaattaccag ctggttggga aaagcactt ccgacataca ctccagaaag ccctgctgat   120

gctacaagaa atctgtctca gcaaaatcta aatgcccttg ttaaggttct tcctggtcta   180

cttggtggca gtgcagatct tgcctcttcc aacatgacct tgttgaaatc atacggagat   240

ttccaa   246

<210>   376
<211>   236
<212>   DNA
<213>   Glycine max

<400>   376

ggatgctaca aggaagaatc ttggatggcc atacgagcct ttccatgtgc cagaagatgt   60

caagaagcat tggagtcgcc atacacctga gggtgctaaa cttgaagctg agtggaatgc   120

caagtttgtg gaatatgaga agcaatacag tgaggaagct gcagagctga aggctattat   180

tactggcgaa ttaccagctg gttgggagaa agcacttccg acatacacac cagaaa   236

<210>   377
<211>   253
<212>   DNA
<213>   Glycine max

<400>   377

attggagtcg ccataccccct gagggtgcta aacttgaagc tgagtggaat gccaagtttg   60

cagaatatga gaagaaatac agtgaggaag ctgcagagct gaaggctatt attactggtg   120

127

aattaccagc tggttgggag aaagcacttc cgacatacac tccagaaagc cctgctgatg   180

ctacaagaaa tctgtctcag caaaatctaa atgccctttt aaggttcttc ctggtctact   240

tggtggcagt gca   253

<210>   378
<211>   250
<212>   DNA
<213>   Glycine max

<400>   378

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gatggccata cgagcctttc catgtgccag aacgtgtcaa gaagcattgg agtcgccata   120

cacctgaggg tgctaaactt gaagctgagt ggaatgccaa gtttgtggaa tatgagaagc   180

aatacagtga ggaagctgca gagctgaagg ctattattac tggcgaatta ccagctggtt   240

gggagaaagc   250

<210>   379
<211>   268
<212>   DNA
<213>   Glycine max

<223>   unsure at all n locations
<400>   379

aaacaaggct aattcctaca gtgttcatng gagtncatta ggtgctaaag aagncgatgc   60

tacaaggnag aatcttggat ggccatacga gcctttccat gtgccagang atgtcaagaa   120

gcattggagt cgccatacac ctgagggtgc taaacttgaa gctgagtgga atgccaagtt   180

tgtggaatat gagaagcaat acagtgaggn agctgcagag tgaaggctat tattactggc   240

gaattaccag ctggttggna nananccct   268

<210>   380
<211>   248
<212>   DNA
<213>   Glycine max

<400>   380

tgctaaagaa gtggatgcta caaggaagaa tcttggatgg ccatacgagc ctttccatgt   60

128

gccaacagat gtcaagaagc attggagtcg ccatacacct gagggtgcta aacttgaagc   120

tgagtggaat gccaagtttg tggaatatga gaagcaatac agtgaggaag ctgcagagct   180

gaaggctatt attactggcg aattaccagc tggttgggag aacgcacttc cgacatacac   240

accagaaa   248

<210>   381
<211>   167
<212>   DNA
<213>   Glycine max

<400>   381

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aaatctaaat gcccttgtta aggttcttcc tggtctactt ggtggtagtg cagatcttgc   120

ctcttccaac atgaccttat tggaatcgta tggggatttc caaaaga   167

<210>   382
<211>   173
<212>   DNA
<213>   Glycine max

<400>   382

atgggagtgc attaggtgct aaagaagtgg atgctacaag gaagaatctt ggatggccat   60

acgagccttt ccatgtgcca gaagatgtac aagagcattg gagtcgccat acacctgagg   120

gtgctaaact tgaagctagt ggaatgccaa gtttgtggaa tatgagaagc aat   173

<210>   383
<211>   298
<212>   DNA
<213>   Glycine max

<223>   unsure at all n locations
<400>   383

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gctaaaagaa gtngatgcta caaggaagaa tcttggatgg ccatacgagc ctttccatgt   120

gccagaagat gtcaagaagc attggagtcg ccatacactg agggtgctaa acttgaagct   180

gagtggaatg ccaagtttgt ggaatatgag aagcaataca gtgaggaagc tgcagagctg   240

aaggctatta tactggcgat taccagctgg ttgggagaaa gcattccgac atacacac   298

129

<210> 384
<211> 273
<212> DNA
<213> Glycine max

<223> unsure at all n locations
<400> 384

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agccccggat tcattccata ctgtgcaact ttctttgtct tcactgacta catgagagct   120

gccataagga tttctgcact gtgtgaagct ggagttatnc nagtgatgac tcatgattcg   180

attggacttg gagaggatgg accaactcat cagccaatag agcacttggc aagcttcagg   240

gcaatgccaa acatttgatg cttcgtccag ctg   273

<210> 385
<211> 295
<212> DNA
<213> Glycine max

<400> 385

gttaggtttg gtgttagaga acatggattg ggagcaatct gtaacggtat tgctcttcat   60

agttccggat tcattccata ctgtgcaact ttctttgtct tcactgacta tatgagagct   120

gccataagga tttctgcact gtgtcgggct ggagttattt atgtgatgac tcatcattcg   180

attggacttg gagaggatgg accaactcat cagccaatag agtatttggc aagcttcagg   240

gcaatgcctc acactttgat gcttcgtcca gctgatgtat atgaactgct ggatc   295

<210> 386
<211> 260
<212> DNA
<213> Glycine max

<400> 386

gcaaaatcta aatgcccttg ttaaggttct tcctggtcta cttggtggta gtgcagatct   60

tgcctcttcc aacatgacct tattgaaatc gtatggggat ttccaaaaga atactcccga   120

agagcgcaat gttaggtttg gtgttagaga acatggaatg ggagcaatct gtaacggtat   180

tgctcttcat agccccggat tcattccata ctgtgcaact ttctttgtct tcactgacta   240

130

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tatgagagct tccataagga                                                      260


        <210>       387
        <211>       249
        <212>       DNA
        <213>       Glycine max

        <400>       387

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gagcgcaatg ttagatttgg tgttagagaa catggaatgg gagcaatctg taatggtatt    120

gctcttcata gccccggatt cattccatac tgtgcaactt tctttgtctt cactgactac    180

atgagagctg ccataaggat ttctgcactg tgtgaagctg gagttatttta tgtgatgact    240

catgattcg                                                            249


        <210>       388
        <211>       252
        <212>       DNA
        <213>       Glycine max

        <400>       388

gggatttcca aaagaatact cccgaagagc gcaatgttag gtttggtgtt agagaacatg    60

gaatgggagc aatctgtaac ggtattgctc ttcatagccc cggattcatt ccatactgtg    120

caactttctt tgtcttcact gactatatga gagctgccat aaggatttct gcactgtgtg    180

aagctggagt tatttatgtg atgactcatg attcgattgg acttggagag gatggaccaa    240

ctcatcagcc aa                                                        252


        <210>       389
        <211>       255
        <212>       DNA
        <213>       Glycine max

        <400>       389

agcagatctt gcctcttcca acatgacctt attgaaatcg tatggggatt tccaaaagaa    60

tactcccgaa gagcgcaatg ttaggtttgg tgttagagaa catggaatgg gagcaatctg    120

taacggtatt gctcttcata gccccggatt cattccatac tgtgcaactt tctttgtctt    180

cactgactat atgagagctg ccataaggat ttctgcactg tgtgaagctg gagttatttta    240
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131

tgtgatgact catga   255

gggagcaatc tgtaatggta ttgctcttca tagccccgga ttcattccat actgtgcaac   60

ttttttttgtc ttcactgact acatgagagc tgccataagg atttctgcac tgtgtgaagc   120

tggagttatt tatgtgatga ctcatgattc gattggactt ggagaggatg gaccaactca   180

tcagccaata gagcacttgg caagcttcag ggcaatgcca aacactttga tgcttcgtcc   240

agctgatggt aatgaaactg   260

ccggattcat tccatactgt gcaactttct ttgtcttcac tgactatatg agagctgcca   60

taaggatttc tgcactgtgt gaagctggag ttatttatgt gatgactcat gattcgattg   120

gacttggaga ggatggacca actcatcagc caatagagca tttggcaagc ttcagggcaa   180

tgccaaacac tttgatgctt cgtccagctg atggtaatga aactgctgga tcatacaa   238

gcaaaatcta aatgcccttg ttaaggttct tcctggtcta cttggtgnnc gtgcagatct   60

tgcctcttcc aacanngacc ttgttgaaat catacggaga tttccaaaag aatactcccg   120

aagagcgcaa tgttagattt ggtgttagag aacatggaat gggagcaatc tgtaatggta   180

ttgcncttca tagccccgga ttcatccata ctgtgcaact tttnttgtct tcatggacta   240

catgagag   248

132

<210> 393
<211> 167
<212> DNA
<213> Glycine max

<400> 393

catgacctta ttgaaatcgt attgggattt ccaaaagact actcccgaag agcgcaatgt   60

taggtttggt gttagagaac atggaatggg agcaatctgt aacggtattg ctcttcatag   120

acccggattc attccatact gtgcaacttt ctttgtcttc actgact   167

<210> 394
<211> 91
<212> DNA
<213> Glycine max

<400> 394

gactacatga gagctgccat aaggatttct gcactgtgtg aaagctggag ttatttatgt   60

gatgactcat ggattcgatt ggacttggag a   91

<210> 395
<211> 288
<212> DNA
<213> Glycine max

<223> unsure at all n locations
<400> 395

tgaattccga caatggggga gcaggactcc tggacatcct gagaactttg agacagttgg   60

aattgaagtg actacaggtc ctcttggtca gggcattgcc aatgctgttg ggttagcact   120

agctgagaaa cacttggctg cacgatttaa caagcctgac aatgagattg ttgaccatta   180

cacatatgtt atattgggtg atggttgtca aatggaggga atttcaaatg aagcatgctc   240

acttgccggt cactggggtc tagggaagct tatngcttta atgatgac   288

<210> 396
<211> 262
<212> DNA
<213> Glycine max

<400> 396

133

caagacctta aggaattccg acaatgggga agcagaactc ctggacatcc tgagaacttt   60

gagacccttg gagttgaagt gaccacaggt cctcttggtc agggcattgc caatgctgtt   120

ggattagcac tagctgagaa gcacttggct gcacgattta acaagcctga caatgagatt   180

gttgaccatt acacatatgt tatattgggt gatggttgtc aaatggaggg aatttcaaat   240

gaagcatgct cacttgccgg tc   262

<210>   397
<211>   279
<212>   DNA
<213>   Glycine max

<223>   unsure at all n locations
<400>   397

cgcttggntc aaccntgacc gtttcgttct ctctgctgga tctggctgca tgctccaata   60

tgctctcctt cancttgctg gctatnacac tgttcaggaa caagacctta aggaattccg   120

acaatgggga agcagaactc ctggacatcc tgagaacttt gagacccttg gagttgaagt   180

gaccacaggt cctcttggtc agggcattgc caatgctgtt ggattagcat agctgagaag   240

cacttggctg cacgattaac aagcctgaca atgagatgt   279

<210>   398
<211>   254
<212>   DNA
<213>   Glycine max

<400>   398

tgacactgtt caggaacaag accttaagga attccgacaa tggggaagca gaactcctgg   60

acatcctgag aactttgaga cccttggagt tgaagtgacc acaggtcctc ttggtcaggg   120

cattgccaat gctgttggat tagcactagc tgagaagcac ttggctgcac gatttaacaa   180

gcctgacaat gagattgttg accattacac atatgttaat tgggtgatgg ttgtcaaatg   240

gagggaattt caaa   254

<210>   399
<211>   264
<212>   DNA
<213>   Glycine max

<400>   399

134

gttgaaaagg gtggttacac catttcggac aactccactg gcaacaagcc tgatgtcatt   60

ttgatcggaa ctggttcgga attggaaatc gctgccaaag ctgctgatga cctaaggaag   120

gaagggaagg ctgttagagt tgtttccctt gtttcttggg aacttttga tgagcaatca   180

gaagcctaca aggagagtgt tttccctgct gctgtttcag ccagagttag cattgaggca   240

ggatcaacat ttgggtggga gaaa   264

<210>   400
<211>   258
<212>   DNA
<213>   Glycine max

<223>   unsure at all n locations
<400>   400

gttgaaaagg gtggttacac catttcggac aactccactg gcaacaagcc tgatgtcatt   60

ttgatcggaa ctggttcgga attggaaatc gctgccaaag ctgctgatga cctaaggaag   120

gaagggaagg ctgttagagt tgtttccctt gtttcttggg aacttttga tgagcaatca   180

gnagcctaca aggagagtgt tttccctgct gctgtttcag ccagagttag cattgaggca   240

ggatcaacat ttgggtgg   258

<210>   401
<211>   249
<212>   DNA
<213>   Glycine max

<400>   401

gagttgaaaa gggtggttac accatttcgg acaactccac tggcaacaag cctgatgtca   60

ttttgatcgg aactggttcg gaattggaaa tcgctgccaa agctgctgat gacctaagga   120

aggaagggaa ggctgttaga gttgtttccc ttgtttcttg gaactttttt gatgagcaat   180

cagaagccta caaggagagt gttttccctg ctgctgtttc agccagagtt agcattgagg   240

caggatcaa   249

<210>   402
<211>   273
<212>   DNA
<213>   Glycine max

135

<400> 402

gagttgaaaa gggtggttac accatttcgg acaactccac tggcaacaag cctgatgtca   60

ttttgatcgg aactggttcg gaattggaaa tcgctgccaa agctgctgat gacctaagga   120

aggaagggaa ggctgttaga gttgtttccc ttgtttcttg gaacttttt gatgagcaat   180

cagaagccta caaggagagt gttttccctg ctgctgtttc agccagagtt agcattgagg   240

caggatcaac atttgggtgg agaaaaattg ttg   273

<210>   403
<211>   256
<212>   DNA
<213>   Glycine max

<400>   403

cactcttctt cttcttcttc ttcttcactc tacaaccact aaactaagtg gttggttttg   60

gtttagtttc attttttga agctcttaaa cttaaggctt aagccatggc atcctcatcc   120

tctctgcatc tatctcaggc ccttctggca cgtgctgtgt accttcatgg ctcttcttct   180

tctgaccgtg tctcactctc cttcccatca ttctctggcc tcaagtcaca ttctgcatgc   240

tccaatatgc tctcct   256

<210>   404
<211>   233
<212>   DNA
<213>   Glycine max

<400>   404

ctaaactaag tggttggttt tggtttagtt tcattttttt gaagcgctta aacttaaggc   60

ttaagccatg gcatcctcat cctctctgca tctatctcag gcccttctgg cacgtgctgt   120

gtaccttcat ggctcttctt cttctgaccg tgtctcactc tccttcccat cattctctgg   180

cctcaagtca cattctacat gcaaagcagc agtagccacg tcctcgcgta gaa   233

<210>   405
<211>   247
<212>   DNA
<213>   Glycine max

<400>   405

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agccatggca tcctcatcct ctctgcatct atctcaggcc cttctggcac gtgctgtgta   120

ccttcatggc tcttcttctt ctgaccgtgt ctcactctcc ttcccatcat tctctggcct   180

caagtcacat tctacatgca aagcagcagc agccacgtcc tcgcgtagaa ggggtgcttg   240

tccatcc   247

<210>   406
<211>   243
<212>   DNA
<213>   Glycine max

<400>   406

aaacactctt cttcttcttc ttcttcttca ctctacaacc actaaactaa gtggttggtt   60

ttggtttagt ttcattttttt tgaagctctt aaacttaagg cttaagccat ggcatcctca   120

tcctctctgc atctatctca ggcccttctg gcacgtgctg tgtaccttca tggctcttct   180

tcttctgacc gtgtctcact ctccttccca tcattctctg cctcaagtc acattctaca   240

tgc   243

<210>   407
<211>   215
<212>   DNA
<213>   Glycine max

<400>   407

ttttggttta gtttcattgt tctgaagctc ttaaacttaa ggcttaagcc atggcatcct   60

catcctctct gcatctatct caggcccttc tggcacgtgc tgtgtacctt catggctctt   120

cttctctgac cgtgtctcac tctccttccc atcattctct ggcctcaagt cacattctac   180

atgcaaagca gcagcagcca cgtcctcgcg tagaa   215

<210>   408
<211>   276
<212>   DNA
<213>   Glycine max

<223>   unsure at all n locations
<400>   408

tcttcttctt cactctacaa ccactannct aagtggttgg ttttggttta gtttcatttt   60

137

tttgaagctc ttaaacttaa ggcttaagcc atggcatcct catcctctct gcatctatct   120

caggcccttc tggcacgtgc tgtgtacctt catggctctt cttcttctga ccgngtctca   180

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acgtcctcgc gtagaagggg tgcttgtcca tccacc   276

<210>   409
<211>   289
<212>   DNA
<213>   Glycine max

<400>   409

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tttcattttt ttgaagctct taaacttaag gcttaagcca tggcatcctc atcctctctg   120

catctatctc aggcccttct ggcacgtgct gtgtacttc atggctcttc ttcttctgac   180

cgtgtctcac tctccttccc atcattctct ggcctcaagt cacattctac atgcaaagca   240

gcagcagcca cgtcctcgcg tagaaggggt gcttgtccat ccaccaacg   289

<210>   410
<211>   221
<212>   DNA
<213>   Glycine max

<223>   unsure at all n locations
<400>   410

tcttcttctt cactctacaa ccactaaact aagtggttgg ntttggttta gtttcatttt   60

tttgaagctc ttaaacttaa ggcttaagcc atggcatcct catcctctct gcatctatct   120

caggcccttc tggcacgtgc tgtgtacctt catggctctt cttcttctga ccgngtctca   180

ctctccttcc catcattctc tggcctcaag tcacattcta t   221

<210>   411
<211>   255
<212>   DNA
<213>   Glycine max

<400>   411

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agtttcattt ttttgaagct cttaaactta aggcttaagc catggcatcc tcatcctctc   120

tgcatctatc tcaggccctt ctggcacgtg ctgtgtacct tcatggctct tcttcttctg   180

accgtgtctc actctccttc ccatcattct ctggcctcaa gtcacattct acatgcaaag   240

cagcagcagc cacgt   255

<210>   412
<211>   333
<212>   DNA
<213>   Glycine max

<223>   unsure at all n locations
<400>   412

anattgtaga ccantanaca tatgtnatat tnggtgatgg ntgtcaaatg gagggantnt   60

caaatgaagc atgctcactt gccggtcact ggggtctagg gaagcttatn gcttnatatg   120

atgacaacca catttccatt gatggggaca ctgagattgc attcactgag aatgttgatc   180

aacgttttga ggcacttggg tggcatgtaa tttgggtgaa gaatggaaat actggatatg   240

atgaaattcg tgcagccatt aaggaagcaa aggctgtcaa agacgaaccc actatgatcc   300

aggtaaccac taccattgga ttggttctcc aaa   333

<210>   413
<211>   260
<212>   DNA
<213>   Glycine max

<400>   413

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caaatggagg gaatttcaaa tgaagcttgc tcacttgccg gtcactgggg tctaggaaag   120

ctcattgctt tatatgatga caatcacatt tccattgatg gtgacactga gattgcattc   180

actgagaatg ttgatcagcg ttttgaagca cttggatggc atgtaatttg ggtgaagaat   240

ggaaatactg gatatgatga   260

<210>   414
<211>   288
<212>   DNA
<213>   Glycine max

<223>   unsure at all n locations

139

cacttggctg cacgatttaa caatcctgnc antgagattg ttgaccatta nacatatgtt   60

atattgggtg atggttgtca aatggaggga atttcaaatg aagcatgctc acttgccgnc   120

tcactggggt ctagggaagc ttattgcttt ntatgatgac aaccacattt ccattnctgg   180

ggacactgag attgcattca ctgagantgt tgatcaacgt ttgaggcact gggtggcat   240

gtaatttggg tgaagaatgg anatactgga tatgatgaaa ttcgtgcg   288

<210>   415
<211>   242
<212>   DNA
<213>   Glycine max

gaatttcaaa tgaagcatgc tcacttgccg gtcactgggg tctagggaag cttattgctt   60

tatatgatga caaccacatt tccattgatg gggacactga gattgcattc actgagaatg   120

ttgatcaacg ttttgaggca cttgggtggc atgtaatttg ggtgaagaat ggaaatactg   180

gatatgatga aattcgtgca gccattaagg aagcaaaggc tgtcaaagac aaacccacta   240

tg   242

<210>   416
<211>   251
<212>   DNA
<213>   Glycine max

caaatggagg gaatttcaaa tgaagcatgc tcacttgccg gtcactgggg tctagggaag   60

cttattgctt tatatgatga caaccacatt tccattgatg gggacactga gattgcattc   120

actgagaatg tgatcaacgt tttgaggcac ttgagtggca tgtaatttgg gtgaagaatg   180

gaaatactgg atatgatgaa attcgtgcag ccattaagga agcaaaggct gtcaaagaca   240

cccactatga t   251

<210>   417
<211>   245
<212>   DNA
<213>   Glycine max

<400>   417

gcacgattta acaagcctga caatgagatt gttgaccatt acacatatgt tatattgggt   60

gatggttgtc aaatggaggg aatttcaaat gaagcatgct cacttgccgg tcactgggt   120

ctagggaagc ttattgcttt atatgatgac aaccacattt ccattgatgg ggacactgag   180

attgcattca ctgagaatgt tgatcaacgt tttgaggcac ttgggtggca tgtaatttgg   240

gtgaa   245

<210>   418
<211>   249
<212>   DNA
<213>   Glycine max

<223>   unsure at all n locations
<400>   418

gttgatcang cgttttgnaa gcacttggat ggcatgtaat ttgggtgaag natggaaata   60

ctggatatga tgaaattgcg tgcagccatt aaagaagnaa aggctgtcaa agacaaaccc   120

actttgatca aggtanccac tagnattgga ttaggttctc caaacaaggc taattcncac   180

agtgttcatg ggncgtgcat taggtgctaa agaagtggat gctacnangn anaatnttgg   240

atggcnata   249

<210>   419
<211>   240
<212>   DNA
<213>   Glycine max

<400>   419

cattgatgca gttgagaagg ccaactctgg tcaccctggt ctccccatgg ggtgtgctct   60

aatgggctca cattctctac gatgagataa tgaggtacaa ttctaagaac cccgcttggt   120

tcaaccgtga cgtttcgttc tctctgctgg acatggctgc atgctccaat atgctctcct   180

tcaccttgct ggctatgaca ctgttcagga acaagacctt aaggaattcc gacaatgggg   240

<210>   420
<211>   283
<212>   DNA
<213>   Glycine max

<400>   420

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caagattgtt ggaagcaaag gaaaggccat aggcattgat cgatttggag caagtgctcc     60

agctggaaaa atatacaagg agtttggtat caccaaggaa gctgttattg ctgctgccaa    120

agaactttcg tagatatatt tgttgagttt cttttatctc atctagaact tgtggttttc    180

acttgtggct ttgggttact gttacatgac ttgttttttg agatatcact ttagccacaa    240

taaggaagat tagatgttct gcatatgatt gtcagaggaa cca                      283


<210>     421
<211>     259
<212>     DNA
<213>     Glycine max

<400>     421

caagattgtt ggaagcaaag gaaaggccat aggcattgat cgatttggag caagtgctcc     60

agctggaaaa atatacaagg agtttggtat caccaaggaa gctgttattg ctgctgccaa    120

agaactttcg tagatatatt tgttgagttt cttttatctc atctagaact tgtggttttc    180

acttgtggct ttgggttact gttacatgac ttgttttttg agatatcact ttagccacaa    240

taaggaagat tagattgtt                                                 259


<210>     422
<211>     256
<212>     DNA
<213>     Glycine max

<400>     422

caagattgtt ggaagcaaag gaaaggccat aggcattgat cgatttggag caagtgctcc     60

agctggaaaa atatacaagg agtttggtat caccaaggaa gctgttattg ctgctgccaa    120

agaactttcg tagatatatt tgttgagttt cttttatctc atctagaact tgtggttttc    180

acttgtggct ttgggttact gttacatgac ttgttttttg agatatcact ttagccacaa    240

taaggaagat tagatt                                                    256


<210>     423
<211>     271
<212>     DNA
<213>     Glycine max

<223>     unsure at all n locations
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142

<400> 423

aaaggaaagg ccataggcat tgatcgattt ggagcaagtg ctccagctgg aaaaatatac 60

aaggagtttg gtatcaccaa ggaagctgtt attgctgctg ccaaagaact ttcgtaatat 120

atttgttgag tntcttttat ctcatctaga acttgtggtt ttcacttgtg ctttgggtt 180

actgttacat gacttgtttt ttgagatatc actttagcca caatanggaa gatagattgt 240

tcttgcatat gattgtcaga ggaaccactt a 271

<210>	424
<211>	258
<212>	DNA
<213>	Glycine max

<223>	unsure at all n locations
<400>	424

tctgcactgt gtgaagctgg agttatttat gtgatgactc atgattcgat tggacttgga 60

gaggatggac caactcatca gccaatagag catttggcaa gcttcagggc aatgccaaac 120

actttgatgc ttgtccagct gatggnaatg aaactgctgg atcatacaaa gttgctgtgg 180

ttaacaggaa gagaccctca attcttgcac tttctaggca aaagttgacc caacttccag 240

ganttctatt gagggagt 258

<210>	425
<211>	209
<212>	DNA
<213>	Glycine max

<400>	425

gctgatggta atgaaactgc tggatcatac aaagttgctg tggttaacag gaagagaccc 60

tcaattcttg cactttctag gcaaaagttg acccaacttc caggaacttc tattgaggga 120

gttgaaaagg gtggctacac catttcagac aactcatcag gtaacaagcc tgatgttatt 180

ttgattggaa ctggttctga gttggaaat 209

<210>	426
<211>	257
<212>	DNA
<213>	Glycine max

<400>	426

cgaccaactc atcagccaat agagcatttg gcaagcttca gggcaatgcc aaacacttag   60

atgcttcgtc cagctgatgg taatgaaact gctggatcat acaaagttgc tgtggttaac   120

aggtagagac cctcaattct tgcactttct aggcaaaagt tgacccaact ccaggaact   180

tctattgagg gatttgaaaa gggtggctac accattctcg aacagctcat caggtaacaa   240

gccggatgtt attttga   257

<210>   427
<211>   246
<212>   DNA
<213>   Glycine max

<400>   427

gctgtggtta acaggaagag accctcaatt cttgcacttt ctaggcaaaa gttgacccaa   60

cttccaggaa cttctattga gggagttgaa aagggtggct acaccatttc agacaactca   120

tcaggtaaca agcctgatgt tattttgatt ggaactggtt ctgagttgga aattgctgct   180

gctgctctg aggatctagg aaaggaagga aaagctgtta gagttgtttc ttttgttagc   240

tgggaa   246

<210>   428
<211>   168
<212>   DNA
<213>   Glycine max

<400>   428

gaccaactca tcagccaata gagcacttgg caagcttcag ggcaatgcca aacactttga   60

tgcttcgtcc agctgatggt aatgaaactg ctggatcata caaagttgct gtggttaaca   120

ggaagagacc ctcaattctt gcactttcta ggcaaaagtt gacccaac   168

<210>   429
<211>   168
<212>   DNA
<213>   Glycine max

<400>   429

aattcttgca ctttctaggc aaaagttgac ccaacttcca ggaacttcta ttgagggagt   60

tgaaaagggt ggctacacca tttcagacaa ctcatcaggt aacaagcctg atgttatttt   120

144

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gattggaact ggttctgagt tggaaattgc tgctgctgct gctgagga                    168


<210>        430
<211>        254
<212>        DNA
<213>        Glycine max

<223>        unsure at all n locations
<400>        430

ctcatgattc gattggactt gggagaggat ggaccaacta catcagccaa tagagcattt    60

ngcaagcttc agggcaatgc caaacacttn cntgcttcgt ccagctatgg taatgaaact    120

gctggatcat acaaagttgc tgtggttaac aggaagagac cctcaattct tgcactttct    180

agncaaaagt tgacccaact tccaggaact tctattggag gtgaaaaggg tggctacacc    240

atttcagana actc                                                      254


<210>        431
<211>        117
<212>        DNA
<213>        Glycine max

<400>        431

aattcttgca cttgctaggc aaaagttgac ccagcttcca ggaacttcta ttgagggagt    60

tgaaaagggt ggctacacca tttcagacaa ctcatcaggt aacaagcctg atgttat       117


<210>        432
<211>        263
<212>        DNA
<213>        Glycine max

<400>        432

atgagaggtg ccataaagct ttctgcgctg tctgaggctg gggttatta atgtcatgac     60

ccatgattca ataggacttg gagaagatgg gccaacccac cagcctattg agcacctagc    120

aagcttccgg gcaatgccaa acattttgat gcttcgtccc gccgacggta acgaaacagc    180

cggagcatac aaagtggccg tgctcaacag gaagagaccc tccattcttg ccctatccag    240

gcaaaaactg ccccagcttc ccg                                            263


<210>        433
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145

<211>   257
<212>   DNA
<213>   Glycine max

<400>   433

cattttgatg cttcgtcctg ccgacggtaa cgaaacagcc ggagcataca aagtggccgt   60

gctcaacagg aagagaccct ccattcttgc cctatccagg caaaaactgc cccagcttcc   120

cggaacttcc attgaaggag ttgaaaaggg tggttacacc atttcggaca actccactgg   180 .

caacaagcct aatgacattt ggaccggaac tggttcggaa ttggaaatcg ctgccaaagc   240

tgctgatgac ctaagga   257

<210>   434
<211>   253
<212>   DNA
<213>   Glycine max

<400>   434

tcatgaccca tgattcaata ggacttggag aagatgggcc aacccaccag cctattgagc   60

acctagcaag cttccgggca atgccaaaca ttttgatgct tcgtcccgcc gacggtaacg   120

aaacagccgg agcatacaaa gtggccgtgc tcaacaggaa gagaccctcc attcttgccc   180

tatccaggca aaaactgccc cagcttcccg gaacttccat tgaaggagtt gaaaagggtg   240

gttacaccat ttc   253

<210>   435
<211>   134
<212>   DNA
<213>   Glycine max

<223>   unsure at all n locations
<400>   435

ttggagaaga tgggccaacc caccagccta ttgagcacct agnnagcttc cgggcaatgc   60

caaacatttt gatgcttcgt cccgccgacg gtaacgaaac agccgnagca taccaagtgg   120

ccgtgtcaac aggg   134

<210>   436
<211>   387
<212>   DNA
<213>   Glycine max

146

<400>   436

cccacgcgtc cgcccacgcg tccgggtcac aacaaccatt ggttatggtt ctcctaacaa   60

ggctaactcc tacagtgtgc atggaagtgc actgggtgcc aaagaagttg atgccacaag   120

gcagaacctt ggatggtcac atgagccatt ccacgtgcct gaggatgtca aaaagcattg   180

gagtcgccac acccctgagg gtgctgcact tgaagctgaa tggaatgcta agtttgctga   240

gtatgaaaag aaatacaagg aggaagctgc agaattgaaa tctattatca atggtgaatt   300

ccctgctggt tgggagaaag cactttcgac atacactcca gagagcccag cggatgccac   360

cagaaacctg tctcaaacaa accttaa   387

<210>   437
<211>   316
<212>   DNA
<213>   Glycine max

<400>   437

ggggttattt atgtcatgac ccatgattca ataggacttg gagaagatgg gccaacccac   60

caccctattg agcacctagc aagcttccgg gcaatgccaa acattttgat gcttcgtccc   120

gccgacggta cgaaacagc cggagcatac aaagtggccg tgctcaacag gaagagaccc   180

tccattcttg ccctgtccag gcaaaaactg ccccagcttc ccggaacttc cattgaagga   240

gttgaaaagg gtggttacac catttcggac aactccactg gcaacaagcc tgatgtcatt   300

ttgatcggaa ctggtt   316

<210>   438
<211>   301
<212>   DNA
<213>   Zea mays

<400>   438

gtcatcttcc acgtctccaa gaccggcggc cacctcgggt ccagcctcgg cgtggtggag   60

ctcaccgtcg cgctgcacta cgtcttcaac gcgccgcagg accgcatcct ctgggacgtc   120

ggccaccagt cgtacccgca caagatcctg acggggcggc gcgacaagat gccgacgatg   180

cggcagacca acggcctggc gggcttcccc aagcgcgccg agagcgagta cgacagcttc   240

ggcacgggcc acagctccac caccatctcc gcggcgctcg ggatggcggt gggccgggac   300

147

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<210>      439
<211>      265
<212>      DNA
<213>      Zea mays

<400>      439

cggtgccgcc caactacaaa ggcactcccc tcgaggtcgg caaaggcagg atcctgcttg   60

agggcgaccg ggtggcgctg ctggggtacg ggtcggcagt gcagtactgc ctgactgccg  120

cgtccctggt gcagcgccac ggcctcaagg tcaccgtcgc cgacgcgagg ttctgcaagc  180

cgctggacca cgccctgatc aggagcctgg ccaagtccca cgaggtgctc atcaccgtgg  240

aggaaggctc catcggcggg ttcgg                                        265


<210>      440
<211>      245
<212>      DNA
<213>      Zea mays

<400>      440

gtgggccggg acctcaaggg cggcaagaac aacgtggtcg cggtgatcgg cgacggcgcc   60

atgacggccg ggcaggcgta cgaggccatg aacaacgccg ggtacctgga ctccgacatg  120

atcgtcatcc tcaacgacaa caagcaggtg tccttgccca cggcgacgct cgacgggccg  180

gtgccgcccg taggcgcgct cagcagcgac ctcagcaagc tgcagtcaag caggccgctc  240

aagga                                                              245


<210>      441
<211>      156
<212>      DNA
<213>      Zea mays

<400>      441

gaagcaggtc ggtggctcag tgcacgagct ggcggcgaag gtggacgagt acgcccgcgt   60

catgatcagc gggcccggct cctcgctctt cgaggagctc ggtctctact acatcggccc  120

cgtcgacggc cacaacatcg acgacctcat caccat                            156
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148

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<210>       442
<211>       271
<212>       DNA
<213>       Zea mays

<400>       442

gtgtacgtga cggtagccga cgcccggttc tgcaagccgc tggacacggc gctgatccgg   60

gagctcgccg ccgagcacga ggtgctgatc accgccgagg agggatccat cggcgggttc  120

ggctcccacg tcgcacacta cctcagcctg accggcctcc tggacgggcc cctcaaactg  180

agatccatgt tcctgccgga ccggtacatc gaccatggcg caccgcagga ccagatcgag  240

gattcagggc tgacgccgcg gcacatcgcc g                                  271


<210>       443
<211>       288
<212>       DNA
<213>       Zea mays

<400>       443

ccgacgcccg gttctgcaag ccgctggaca cggcgctgat ccgggagctc gccgccgagc   60

acgaggtgct gatcaccgcc gaggagggat ccatcggcgg gttcggctcc cacgtcgccc  120

actacctcag cctgaccggc ctcctggacg gcccctcaa actgagatcc atgttcctgc  180

cggaccggta catcgaccat ggcgcaccgc aggaccagat cgatgaggca gggctgacgc  240

gcggcacatc gccgccaccg tgctgtccct gctggggagg ccattgga                288


<210>       444
<211>       340
<212>       DNA
<213>       Zea mays

<400>       444

aagagcacca agaccaccgg ccccgtcctc atccacgtcg tcaccgagaa gggccgcggc   60

taccccctacg ccgagcgagc cgccgacaag taccacggtg tcgccaagtt tgatccggcg  120

accgggaagc agttcaagtc ccccgccaag acgctgtcct acaccaacta cttcgccgag  180

gcgctcatcg ccgaggcggg ccaggacagc aagatcgtgg ccatccacgc ggccatgggc  240

ggcggcacgg ggctcaacta cttcctccgc cgcttcccga accggtgctt cgacgtcggg  300

atcgcggaca gcacgccgtc acgttcgggc cggctggctg                        340
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149

<210>   445
<211>   245
<212>   DNA
<213>   Zea mays

<400>   445

gtaccacggt gtcgccaagt ttgatccggc gaccgggaag cagttcaagt cccccgccaa   60

gacgctgtcc tacaccaact acttcgccga ggcgctcatc gccgaggcgg agcaggacag   120

caagatcgtg gccatccacg cggccatggg cggcggcacg gggctcaact acttcctccg   180

ccgcttcccg agccggtgct tcgacgtcgg gatcgcggag cagcacgccg tcacgttcgc   240

ggccg   245

<210>   446
<211>   298
<212>   DNA
<213>   Zea mays

<223>   unsure at all n locations
<400>   446

cgatctgcag aagctaccgg taaggttcgt catggacagg gccgggctgg tcggcgcgga   60

cgggccgacc cactgcgggg cgttcgacgt cgcgtacatg gcctgcctgc ccaacatggt   120

cgtcatggcc ccgtccgacg aggccgagct ctgccacatg gtcgccaccg ccgcggcaat   180

cgacgaccgc ccgtcctgct tccgctaccc gagaggcaac ggcgttggcg tcccgttgcc   240

gnccaactac aaaggcactc ccctcgaggt cgggcaaagc aggatcctgc tggagggc   298

<210>   447
<211>   333
<212>   DNA
<213>   Zea mays

<223>   unsure at all n locations
<400>   447

cagggccggg ctggtcggcg cggacgggcc gacccactgc ggggcgttcg acgtcgcgtg   60

catggcctgc ctgcccaaca tggtcgtcat ggccccgtcc gacgaggccg agctctgcca   120

catggtcgcc accgccgcgg caatcgacga ccgcccgtcc tgcttccgct acccgagagg   180

caacggcgtt ggcgtcccgt tgccgcccaa ctacaaaggc actcccctcg aggtcggcaa   240

150

aggcaggatc ctgctggagg gcgacaccgg ggngctgctg gngtacgggt cgggagtgca   300

gnactggctg accgtcgcgt acctggtgca gcg   333

<210>   448
<211>   240
<212>   DNA
<213>   Glycine max

<400>   448

caacaagcag gtttctttac caactgctac tcttgatgga cccataccac ctgtaggagc   60

cttgagtagc gctctcagta gattacaatc aaataggcct cttagagaat tgagagaggt   120

tgccaaggga gttcctaaac gaattggagg tcctatgcat gaattggctg caaaagttga   180

cgagtatgct cgtggcatga tcagtggttc tggatcatca cttttgaag agcttggact   240

<210>   449
<211>   309
<212>   DNA
<213>   Glycine max

<400>   449

aatgcagggt accttgactc taacatgata attatactta atgacaacaa gcaagtttct   60

ttgcctactg ctactattga tggtcctgca actccaattg agcccgcaa tagtgcctta   120

agcaaaattc aagcaagcac caaataccgc aaactgagag aagctgcgaa aggcatcaca   180

aagcagatag gaggaacaac acacaacttg cagcaaaggt agatgagtat gcaagaggta   240

tgatcagtgg ttctagtact acacttgttg aggagctcgg cttatactac atatgccctg   300

tggatggtc   309

<210>   450
<211>   233
<212>   DNA
<213>   Glycine max

<400>   450

aaaacaactg gtcctgtgct gctccatgtt gtcactgaaa aaggccatgg atatccatat   60

gcagaaagag cagcagatta gtaccatgga gttactaagt ttgatccatt aactggaaaa   120

caattcaaat tcaatgctgc cacccagtta tacacaacat actttgcaga ggctttaatt   180

151

tctgaagcgg aagcttacaa agacattgtc ggaatccatg ctgcaatggg agg   233

<210>   451
<211>   268
<212>   DNA
<213>   Glycine max

<400>   451

tgtgattctg tatgatagcc gtcactcttt acttccaaaa attgaggagg gcccaaagac   60

atttgtcaat gccctatcta gtaccctgag caagctccag tccagtaaat ctttccggag   120

atttagagaa gctgctaggg gtgttacgaa acgaattggt aggtctgcat gaattggcag   180

ctaaagtgga tgaatatgct cgtggtatga tgggtcctct aggtgctact ctttttgaag   240

agcttgggtt gtactacata ggcccagt   268

<210>   452
<211>   162
<212>   DNA
<213>   Glycine max

<400>   452

cttccttgtt ggaacatcat ggcttgcgcg caacagtggc tgatgcacgt ttctgcaagc   60

cattggaccg ttctcttatt cttagccttg cccaatcgca cgaggttttg atcactgtgg   120

aagaagggca ataggaggat tcggatctca tgttgttcag tt   162

<210>   453
<211>   232
<212>   DNA
<213>   Glycine max

<400>   453

gatctctccg ctctctcatc ataccgcact ctcgggtagt tacttcctct tccctctcac   60

tctcaatggg gtctccattt cctcgcccac gctcaccgcc tccaccagat gaagaaaagg   120

ccatgtgggg tatatgcatc cctctccgag agtggagagt attattccca ccgaccgcca   180

actcccctac tagacaccgt caactatcct attcatatga agaatctctc tg   232

<210>   454
<211>   280

152

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<212>       DNA
<213>       Zea mays

<400>       454

gtgcaccgac caagaaaacc tcgcttcacg atctctacga gctccagggc ctctccccgt   60

ggtatgacaa cctctgccga cctgtcaccg acttgctgcc ccttatcgcc agctgtgttc  120

gtggagtcac cagcaaccct gcagtaatcc tccgtttcca ccttttgttt cttcgcttgc  180

atggttgctg cgcattcact cctgaccgtg tcctcgacgc aatgcagatt ttccagaagg  240

ccatctcatc ctccagcgca tatgatgatc agttcaagca                        280


<210>       455
<211>       274
<212>       DNA
<213>       Zea mays

<400>       455

tgacactcaa ggaactgttg aggaggcaaa gtggttacac aaagtggtca accgccccaa   60

tgtctacata aagatccctg ctaccgcaga atgtgttcat tccatccgtg aagttatcgc  120

taatggcatt agcgtcaacg tcacgcttat attctctatt gcgagatacg aggctgtgat  180

tgatgcttac cttgatgggc tagaggcttc tggcttgagc gacttatctc gagttaccag  240

tgtcgcatcc ttctttgtca gtcgagtcga cacc                              274


<210>       456
<211>       306
<212>       DNA
<213>       Zea mays

<400>       456

ccaacgagca aaccccccat ttgccaccaa ccccgacgag cggcgatgac cggcacgtgt   60

ctaagctggc ggcgccccgt ccggcggcac cgccgctccg gccggcgtcc ctccgcaccg  120

ccgccctcgc cttcgccccc tccgcgcgcc gggtccgcgt ctccgtcgcc gggcgagcca  180

ggagccccat cattgcgatg gcttcggcca aggaaggaaa tggtgcaccg accaagagga  240

ctgcgcttca tgatctctac gagctccagg gcctgtcccc gtggtacgac aacctatgcc  300

gccctg                                                             306
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<210>   457
<211>   330
<212>   DNA
<213>   Zea mays

<400>   457

ccaaggtggg aggcgttggc caagaaaggt gccaagaaac aaaggttgtt gtgggcatcc   60

accggtgtca agaacccagc ttatcctgac actctttatg tggacagtct catcggacct   120

gacacggtca acacgatgcc cgaccaagct ttgcaagcat tcatagacca cggcaccgtt   180

tcaaggacag ttgatgcgaa cgtgtctgag gcggaaggtg tatacagtgc cttggagaag   240

cttggcatcg actgggaaga ggttggaaag cagcttgagc tggaaggcgt ggactccttc   300

aagaagagct ttgacagcct actcgtgagc   330

<210>   458
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<400>   458

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tctcattgga cctgacacgg tcaacacgat gcccgaccaa gctttgcacg cattcataga   180

ccacggcact gtctcgagga cagttgatgc gaatgtgtcc gaggcggaag gtgtatacag   240

cgccttggag aagcttggca ttgactgggg cgaggtcgga aagcagcttg agctggaagg   300

tgtggactcc ttcaaga   317

<210>   459
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<213>   Zea mays

<400>   459

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gtcaacacga tgcccgacca agctttgcaa gcattcatag accacggcac cgtttcaagg   180

acagttgatg cgaatgtgtc tgaggcggaa ggtgtataca gcgccttgga gaagcttggc   240

154

atcgactggg aagaggttgg aaagcagctt gagctggaga gcgtggactc cttcaagaag   300

agcttt   306

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<212>   DNA
<213>   Zea mays

<400>   460

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ccttatcgac aaaatgcttg agaagattgg aacacctgag gcacttgcct tgagagggaa   120

ggctgccgtc gcacaggcca aactagcaaa tcggctctac cagaagaaat tctctggccc   180

gaagtgggag gcgttggcca agaaaggtgc caagaaacag aggttgttgt gggcgtccac   240

cggtgtcaag aacccagctt atcccgacac tctttacatc gacagtctca ttggacctg   299

<210>   461
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<212>   DNA
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<400>   461

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tgacactctt tatgtggaca gtctcatcgg acctgacacg gtcaacacga tgcccgacca   180

agctttgcaa gcattcatag accacggcac cgtttcaagg acagttgatg cgaacgtgtc   240

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<210>   462
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<400>   462

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tcgacaaaat gcttgagaag attggaacac ctgaggcact gccttgaga gggaaggctg   120

ccgtcgcaca ggccaaacta gcaaatcggc tctaccagaa gaaattctct ggcccgaggt   180

155

gggaggcgtt ggccaagaaa ggtgccaaga aacagaggtt gttgtgggca tccaccggtg   240

tcaagaaccc agcttatccc gacactcttt acatcgacag tctcattgga cctga   295

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<400>   463

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ttctggactt gagtgactta tcccgagtta ctagcgttgc atccttcttt gtcagccgag   180

tggacaccct tattgacaaa atgcttgaca agattggaac acctgaggcc cttgccttga   240

gaggaaaggc tgcagtagcg caggccaaac tagcaaatcg gctctaccag aagaaattct   300

ctggcccaag gtg   313

<210>   464
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<212>   DNA
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<400>   464

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ccaagaaaca aaggttgttg tgggcatcca ccggtgtcaa gaacccagct tatcctgaca   180

ctctttatgt ggacagtctc atcggacctg acacggtcaa cacgatgccc gaccaagctt   240

tgcaagcatt catagaccac ggcaccgttt caagg   275

<210>   465
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<212>   DNA
<213>   Zea mays

<400>   465

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ggcttgagcg acttatctcg agttaccagt gtcgcatcct tctttgtcag ccgagtcgac   120

156

accccttatcg acaaaatgct tgagaagatt ggaacacctg aggcacttgc cttgagaggg   180

aaggctgccg tcgcacaggc caaactagca aatcggctct accagaagaa attctctggc   240

ccgaggtggg aggcgttggc caagaaaggt gccaagaaac agaggt   286

<210>   466
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<212>   DNA
<213>   Zea mays

<400>   466

ctcaaggaac tgttgaagcg gcaaagtggt tacacaaagt ggtcaaccgc cccaatgtct   60

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gcattagcgt caacgtcacg cttattttct caattgcgag atatgaggct gtgattgatg   180

cttacctcga tgggctagag gcttctggct tgagtgactt atcccgagtt actagcgttg   240

catccttctt tgtcagccga gtggacaccc ttattgacaa aatg   284

<210>   467
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<212>   DNA
<213>   Zea mays

<400>   467

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gaagttatcg ctaatggcat tagcgtcaac gtcacgctta ttttctctat tgcgagatac   120

gaggctgtga ttgatgctta ccttgatggg ctagaggctt ctggcttgag cgacttatct   180

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cttgagaaga ttggaacacc tgaggcactt gccttga   277

<210>   468
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tcctaggttg gcaaatgaca ctcaaggaac tgttgaggcc gcaaagtggt tacacaaagt   120

157

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ggtcaaccgc cccaatgtct acataaagat ccctgctacc gccgaatgtg ttccttccat   180

ccgggaagtt atcgctaatg gcattagcgt caacgtcacg cttattttct ctattgcgag   240

atacgaggct gtgattgatg cttaccttga tgggctaga                          279
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<210>      469
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<212>      DNA
<213>      Zea mays

<400>      469
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gacgcggaga gcgcttactg ggaactcgtt ataaaggata tccaagatgc gtgcaaactt   120

tttgagccca tctacgatga gactgatggg gctgatgggt atgtctccgt agaggtgtct   180

cctaggttgg caaatgacac tcaaggaact gttgaagcgg caaagtggtt acacaaagtg   240

gtcaaccgcc ccaatgtcta cataaagatc ccagctactg cagaatgtgt tccttccatc   300

caggaagtta tcgctaatgg cattagcgtc aacg                               334
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gatatccaag atgcgtgcaa acttttttgag cccatctacg acgagactga tggggctgat   120

gggtatgtct ccgtagaggt gtctcctagg ttggcaaatg acactcaagg aactgttgaa   180

gcggcaaagt ggttacacaa agtggtcaac cgccccaatg tctacataaa gatcccagct   240

actgcagaat gtgttccttc catccaggaa gttatcgcta atggcattag cgtcaacgtc   300

acgcttattt tctcaattgc ga                                            322
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<213>      Zea mays

<400>      471
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158

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cagtctcatt ggacctgaca cggtcaacac gatgcccgac caagctttgc acgcattcat   120

agaccacggc actgtctcga ggacagttga tgcgaatgtg tccgaggcgg aaggtgtata   180

cagcgccttg gagaagcttg gcattgactg gggcgaggtc ggaaagcagc ttgagctgga   240

aggtgtggac tccttcaaga agagctttga cagcctactc gtg                     283


<210>      472
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<212>      DNA
<213>      Zea mays

<400>      472

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aggctgccgt cgcacaggcc aaactagcaa atcggctcta ccagaagaaa ttctctggcc   120

cgaggtggga ggcgttggcc aagaaaggtg ccaagaaaca gaggttgttg tgggcatcca   180

ccggtgtcaa gaacccagct tatcccgaca ctctttacat cgacagtctc attggacctg   240

acacggtcaa cacgatgccc gacca                                         265


<210>      473
<211>      240
<212>      DNA
<213>      Zea mays

<400>      473

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actagcaaat cggctctacc agaagaaatt ctctggccca aggtgggagg cgttggccaa   120

gaaaggtgcc aagaaacaaa ggttgttgtg ggcatccacc ggtgtcagga acccagctta   180

tcctgacact ctttatgtgg acagtctcat cggacctgac acggtcaaca cgatgcccga   240


<210>      474
<211>      301
<212>      DNA
<213>      Zea mays

<400>      474

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159

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aaactttttg agcccatata cgatgagact gatagggctg atgggtatgt ctccgtagag    120

gtgtctccta ggttggcaaa tgacactcaa ggaactgttg aagcggcaaa gtggttacac    180

aaagtggtca accgccccaa tgtctacata aagatcccag ctactgcaga atgtgttcct    240

tccatccagg aagttatcgc taatggcatt agcgtcaacg tcacgcttat tttctcaatt    300

g                                                                    301


<210>        475
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<212>        DNA
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<400>        475

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ccgagtcgac acccttatcg acaaaatgct tgagaagatt ggaacacctg aggcacttgc    120

cttgagaggg aaggctgccg tcgcacaggc caaactagca aatcggctct accagaagaa    180

attctctggc ccgaggtggg aggcgttggc caagaaaggt gccaagaaac agaggttgtt    240

gtgggcatcc accggtgtca agaacccagc ttatcccgac actctttaca tcgacagtct    300


<210>        476
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<212>        DNA
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ccccaatgtc tacataaaga tcccagctac tgcagaatgt gttccttcca tccaggaagt    120

tatcgctaat ggcattagcg tcaacgtcac gcttattttc tcaattgcaa gatatgaggc    180

tgtgattgat gcttacctcg atgggctaga ggcttctggc ttgagtgact tatcccgagt    240

tactagcgtt gcatccttct ttgtcag                                        267


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<400>        477
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160

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acttttgag cccatctacg acagagactga tggggctgat gggtatgtct ccgtagaggt 120

gtctcctagg ttggcaaatg acactcaagg aactgttgaa gcggcaaagt ggttacacaa 180

agtggtcaac cgccccaatg tctacataaa gatcccagct actgcagaat gtgttccttc 240

catccaggaa gttatcgcta atggcattag cgtcaacgtc acgcttttct caa   293

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<212>   DNA
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<400>   478

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aacccagctt atcgcgacac tctttacatc gacagtctca ttggacctga cacggtcaac 120

acgatgcccg accaagcttt gcacgcattc atagaccacg gcactgtctc gaggacagtt 180

gatgcgaatg tgtccgaggc ggaaggtgta tacagcgcct tggagaagct tggcattgac 240

tggggcgagg tcggaaa   257

<210>   479
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<213>   Zea mays

<400>   479

cccttatcga caaaatgctt gagaagattg gaacacctga ggcacttgcc ttgagaggga   60

aggctgccgt cgcacaggcc aaactagcaa atcggctcta ccagaagaaa ttctctggcc 120

cgaggtggga ggcgttggcc aagaaaggtg ccaagaaaca gaggttgttg tgggcgtcca 180

ccggtgtcaa gaacccagct tatcccgaca ctctttacat cgacagtct   229

<210>   480
<211>   263
<212>   DNA
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161

gaactgttga agcggcaaag tggttacaca aagtggtcaa ccgccccaat gtctacataa   120

agatcccagc tactgcagaa tgtgttcctt ccatccagga agttatcgct aatggcatta   180

gcgtcaacgt cacgcttatt ttctcaattg caagatatga ggctgtgatt gatgcttacc   240

tcgatgggct agaggcttct ggc   263

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<212>   DNA
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<400>   481

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cagggcctgt ccccgtggta cgacaaccta tgccgccctg tcacagactt gctgcccatt   120

atcgccagcg ggtccgtgga gtcaccagca acccaacgat tttccaaaag gccatttcat   180

cgtccagcgc atatgatgat cagttcaagc agctcatttc ggcaggaaag gatgcggaga   240

gcgcttactg ggaactcgtt ataaaggata tccaagatgc gtgcaaactt tttgagccca   300

<210>   482
<211>   312
<212>   DNA
<213>   Zea mays

<400>   482

tccaaccaag ggttcggaaa gtcaaggcta atttccccaa tgtgggaaac cgaggctggg   60

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agtgtcgcat ccttctttgt cagtcgagtc gacaccctta tcgacaaaat gcttgagaag   180

attggaacac ctgaggcact tgccttgaga gggaaggctg ccgtcgcaca ggccaaacta   240

gcaaatcggc tctaccagaa gaaattctct ggcccgaggt gggaggcgtt ggccaagaaa   300

ggtgccaaga aa   312

<210>   483
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<213>   Zea mays

<400>   483

162

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agcagctcat ttcggcagga aaggatgcgg agagcgctta ctgggaactc gttataaagg   120

atatccaaga tgcgtgcaaa cttttgagc ccatctacga cgagactgat ggggctgatg   180

ggtatgtctc cgtagaggtg tctcctaggt tggcaaatga cactcaagga actgttgaag   240

cggcaaagtg gttacacaaa gtgg                                          264


<210>      484
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<212>      DNA
<213>      Zea mays

<400>      484

ggtcaacacg atgcccgacc aagctttgca ggcattcata gaccacggca ctgtttcgag    60

gacagttgat gcgaatgtgt ccgaggcgga aggtgtatac agcgccttgg agaagcttgg   120

cattgactgg ggcgaggtcg gaaagcagct tgagctggaa ggtgtggact ccttcaagaa   180

gagctttgac agcctactcg tgagcctgca ggagaagggc aactagcctc aa            232


<210>      485
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<212>      DNA
<213>      Zea mays

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ggtgtctcct aggttggcaa atgacactca aggaactgtt gaagcggcaa agtggttaca   120

caaagtggtc aaccgcccca atgtctacat aaagatccca gctactgcag aatgtgttcc   180

ttccatccag gaagttatcg ctaatggcat tagcgtcaac gtcacgctta ttttctcaat   240

tgcgagatat gaggctgt                                                 258


<210>      486
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<212>      DNA
<213>      Zea mays

<400>      486

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163

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cgaatgtgtt cattccatcc gtgaagttat cgctaatggc attagcgtca acgtcacgct   120

tattttctct attgcgagat acgaggctgt gattgatgct taccttgatg ggctagaggc   180

ttctggcttg agcgacttat ctcgagttac cagtgtcgca tccttctttg tcagtcgagt   240

cgacaccctt atcgacaaaa tgttgagaag atggaacacc tgaggcattg ccttgagagg   300

gaaggtgccg tcgcacagcc aactagca                                       328


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<212>        DNA
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<400>        487

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agcaaccctg caattttcca gaaggccatc tcatcctcca gcgcatatga tgatcagttc   120

aagcagctca tttcgggcgg aaaggacgcg gagagcgctt actgggaact tgttataaag   180

gatatccaag acgcgtgcag tcttttgag cctatctacg atgagaccga tggggctgat   240

gggtatgtct ccgtggaggt gtctcctagg ttgg                                274


<210>        488
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<400>        488

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gggaaggctg agcgtcgcac aggccaaact agcaaatcgg ctctaccaga agaaattctc   120

tggcccgagg tgggaggcgt tggccaagaa aggtgccaag aaacagaggt tgttgtgggc   180

gtccaccggt gtcaagaacc cagcttatcc cga                                 213


<210>        489
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<212>        DNA
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<400>        489

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cggagagcgc ttactgggaa ctcgttataa aggatatcca agatgcgtgc aaactttttg   120

agcccatcta cgatgagact gatggggctg atgggtatgt ctccgtagag gtgtctccta   180

ggttggcaaa tgacactcaa ggaactgttg aagcggcaaa gtggttacac aaagtggtca   240

accgccccaa tgtctacata aa   262

<210>   490
<211>   252
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<213>   Zea mays

<400>   490

cgatggggct gatgggtatg tctccgtgga ggtgtctcct aggttggcaa atgacactca   60

aggaactgtt gaggcggcaa agtggttaca caaagtggtc aaccgcccca atgtctacat   120

aaagatccct gctaccgccg aatgtgttcc ttccatccgg gaagttatcg ctaatggcat   180

tagcgtcaac gtcacgctta ttttctctat tgcgacatac gaggctgtga ttgatgctta   240

ccttgatggg ct   252

<210>   491
<211>   239
<212>   DNA
<213>   Zea mays

<400>   491

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caagcagctc atttcggctg gaaaggacgc ggagagcgct tactgggaac tcgttataaa   120

ggatatccaa gatgcgtgca acttttga gcccatctac gatgagactg atggggctga   180

tgggtatgtc tccgtagagg tgtctcctag gttggcaaat gacactcaag gaactgttg   239

<210>   492
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<212>   DNA
<213>   Zea mays

<400>   492

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tcctgacact ctttatgtgg acagtctcat cggacctgac acggtcaaca cgatgcccga   120

165

ccaagctttg caagcattca tagaccacgg caccgtttca aggacagttg atgcgaacgt 180

gtctgaggcg gaaggt 196

<210> 493
<211> 355
<212> DNA
<213> Zea mays

<223> unsure at all n locations
<400> 493

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anaaggccat ttcatcgtcc agcgcatatg atgatcagtt caagcagctc atttcggctg 180

gaaaggacgc ggagagcgct tactgggaac tcgttataaa ggatatccaa gatgcgtgca 240

aacttttttga gcccatctac gatgagactg atggggctga tgggtatgtc tccgtagagg 300

tgtctcctag gttggcaaat gacactcaag gaactgttga agcggcatag tggtt 355

<210> 494
<211> 270
<212> DNA
<213> Zea mays

<400> 494

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aaggccattt catcgtccag cgcatatgat gatcagttca agcagctcat ttcggcagga 120

aaggatgcgg agagcgctta ctgggaactc gttataaagg atatccaaga tgcgtgcaaa 180

cttttttgagc ccatctacga cgagactgat ggggctgatg ggtatgtctc cgtagaggtg 240

tctcctaggt tggcaaatga cactcaagga 270

<210> 495
<211> 226
<212> DNA
<213> Zea mays

<400> 495

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166

tttgagccca tctacgatga gactgatggg gctgatggt atgtctccgt agaggtgtct   120

cctaggttgg caaatgacac tcaaggaact gttgaagcgg caaagtggtt acacaaagtg   180

gtcaaccgcc ccaatgtcta cataaagatc ccagctactg cagaat   226

<210>   496
<211>   234
<212>   DNA
<213>   Zea mays

<400>   496

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ataaaggata tccaagatgc gtgcaaactt tttgagccca tctacgacga gactgatggg   120

gctgatggt atgtctccgt agaggtgtct cctaggttgg caaatgacac tcaaggaact   180

gttgaagcgg caaagtggtt acacaaagtg gtcaaccgcc ccaatgtcta cata   234

<210>   497
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<213>   Zea mays

<400>   497

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caaggaagga agcggtgcac cgaccaagag gactgcgctt catgatctct acgagctcca   120

gggcctgtcc ccgtggtacg acaacctatg ccgccctgtc acagacttgc tgcccattat   180

cgccagcggc gtccgtggag tcaccagcaa cccaacgatt ttccaaaagg ccatttcatc   240

gtccagcgca tatgatgatc agttcaagca gctcatttcg gcaggaaagg atgcggagag   300

cgcttactgg gaa   313

<210>   498
<211>   243
<212>   DNA
<213>   Zea mays

<400>   498

ggatatgcaa gatgcgtgca aactttttga gcccatctat gacgagactg atggggctga   60

tgggtatgtc tccgtagagg ggtctcctag gttggctaat gacactcaat gtactgttga   120

167

agctgcaaag tggttacaca aagttgtcaa ccgcccaat gtctacataa agatcccagc 180

tactgcagaa tgtgttcctt ccatccagga agttatccct aatggcatta gcgtcaacgt 240

cac 243

<210> 499
<211> 281
<212> DNA
<213> Zea mays

<400> 499

cacgcttatt ttctctattg cgacatacga ggctgtgatt gatgcttacc ttgatgggct 60

agaagcttcg ggcttgagcg acttatctcg agttaccagt gtcgcatcct tctttgtcag 120

ccgagtcgac acccttatcg acaaaatgct gaaaatattg gaacacctga ggcacttgcc 180

ttgagaggga aggctgccgt cgcacaggcc aaactagcaa atcggctcta ccagaagaaa 240

ttctctggcc caaggtggga ggcgttggcc aagaaaggtg c 281

<210> 500
<211> 320
<212> DNA
<213> Zea mays

<400> 500

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accacggcac tgtctcgagg acagttgatg cgaatgtgtc cgatgcggaa cgtgtataca 120

gcgccttgga gaatcttggc attgactggg gcgatgtcgg aaagcagctt gagctggaag 180

gtgtggactc cttcaagaag agctttgaca gcctactcgt gagcctacag gagaatggca 240

acagcctcaa gacggcaact gtgtaaaact gagaagattg ggtagcggcg ggtgaacgat 300

tttactatat aaaatgctag 320

<210> 501
<211> 318
<212> DNA
<213> Zea mays

<400> 501

tgttggccaa gcaagagtgc caacgaaaca gcacgttcgc tgtagcgcat cccttggtgt 60

168

ccagaaccca gcttgtcccg cgactaccta catcgacagt ctcattgggc ctgacacggt   120

caacacgatg cccgaccaag ctttgcacgc attcatagac cacggcactg tctcgaggac   180

agttgatgcg aatgtgtccg aggcggaagg tgtatacagc gccttggaga agcttggcat   240

tgactcgggc gaggtcggaa agcagcttga gctggaaggt gtggactctt caagcagact   300

ttgacagcct actcgtga   318

<210>   502
<211>   283
<212>   DNA
<213>   Zea mays

<400>   502

cagacgcgtg gggtccgcgt ctccgtcgcc gggcgagcca ggagccccat cattgcgatg   60

gcttcggcca aggacggaaa tggtgcaccg accaagagga ctgcgcttca tgatctctac   120

gagctccagg gcctgtcccc gtggtacgac aacctatgcc gccctgtcac agacttgctg   180

cccattatcg ccagcggcgt ccgtggagtc accagcaacc caacgatttt ccaaaaggcc   240

atttcatcgt ccagcgcata tgatgatcag ttcaagcagc tca   283

<210>   503
<211>   275
<212>   DNA
<213>   Zea mays

<400>   503

atctcatcct ccagcgcata tgatggttat ctggaccatt gcagggttgc tggtgactcc   60

acgaacaccg ctattttcca gaaggtcatc tcatcctcca gcgcatatga tgatcagttc   120

aagcagctca tttcgggcgg aaatgacgcg gagagtgctt actgcgaact tgttatacag   180

gatatccaag acgcgtgcag tcttttttgag cctatctacg atgagaccga tggggctgat   240

gggtatgtct ccgtggaggt gtctcctagg ttggc   275

<210>   504
<211>   184
<212>   DNA
<213>   Zea mays

<400>   504

169

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accagcaacc ctacaatttt ccagaaggcc atctcatcct ccagcgcata tgatgatcag    60

ttcaagcagc tcatttcggg cggaaaggac gcggagagcg cttactggga actcgttata   120

aaggatatcc aagacgcgtg cagtcttttt gagcctatct acgatgagac cgatggggct   180

gatg                                                                184


<210>        505
<211>        262
<212>        DNA
<213>        Zea mays

<223>        unsure at all n locations
<400>        505

cccacgcgtc cgatgtgtct gaggcggaag gtgtatacag cgccttggag aagcttggca    60

tcgactggga agaggttgga aagcagcttg agctggaagg cgtggactcc ttcaagaaga   120

gctttgacag cctactcgtg agcctgcagg agaagggcaa cagcctcaag atggcgagtg   180

tgtaaagctg agaagattgg gtacctgcga gtgaacgatt ttactanata naatgctagc   240

ttgctggctc tcctcttagt tt                                             262


<210>        506
<211>        291
<212>        DNA
<213>        Zea mays

<400>        506

cggctcgagg tttcaaggac agttgatgcg aacgtgtctg aggcggaagg tgtatacagt    60

gccttggaga agcttggcat cgactgggaa gaggttggaa agcagcttga gctggaaggc   120

gtggactcct tcaagaagag ctttgacagc ctactcgtga gcctgcagga gaagggcaac   180

agcctcaaga tggcgagtgt gtaaagctga gaagattggg tacctgcgag tgaacgattt   240

tactaaataa aatgctagct tgctggctct cctcttagtt tttacgctgt a            291


<210>        507
<211>        244
<212>        DNA
<213>        Zea mays

<400>        507

aaggcggaag gtgtatacag cgccttggag aagcttggca ttgactgggc cgaggtcgga    60
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170

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aagcagcttg agctggaagg tgtggactcc ttcaagaaga gctttgacag cctactcgtg   120

agcctgcagg agaagggcaa cagcctcaag acggcaactg tgtaaaactg agaagattgg   180

gtaccggcgg gtgaacgatt ttactaaata aaatgctagc ttgctggctc tcctaatttt   240

tacg                                                                244


<210>        508
<211>        298
<212>        DNA
<213>        Zea mays

<400>        508

tgcgaacgtg tctgaggcgg aaggtgtata cagtgccttg gagaagcttg gcatcgactg    60

ggaagaggtt ggaaagcagc ttgagctgga aggcgtggac tccttcaaga agagctttga   120

cagcctactc gtgagcctgc aggagaaggg caacagcctc aagatggcga gtgtgtcaag   180

ctgagaagat tgggtacctg cgagtgaacg attttactaa ataaaatgct agcttgctag   240

ctctcctctt agttttttacg ctgtaccttt gctctcaatt ttctgagtcg gctttgta    298


<210>        509
<211>        241
<212>        DNA
<213>        Zea mays

<400>        509

gcagaatgtg ttccttccat ccaggaagtt atcgctaatg cattagcgt caacgtcacg    60

cttatttttct caattgcaag atatgaggct gtgattgatg cttacctcga tgggctagag   120

gcttctggct tgagtgaatt atcccgagtt actagcgttg catccttctt tgtcagccga   180

gtggacaccc ttattgacaa aatgcttgac aagattggaa cacctgaggc ccttgccttg   240

a                                                                   241


<210>        510
<211>        139
<212>        DNA
<213>        Zea mays

<400>        510

caagacgcgt gcagtctttt tgagcctatc tacgatgaga ccgatggggc tgatgggtat    60
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171

gtctccgtgg aggtgtctcc taggttggca aatgacactc aaggaactgt tgaggccgca 120

aagtggttac acaaagtgg 139

<210>   511
<211>   170
<212>   DNA
<213>   Zea mays

<223>   unsure at all n locations
<400>   511

cggcactgtc tcgaggacag ttgatgcgaa tgtgcccgac gcggaaggtg tatacagcgc 60

cttggagaag cttggcattg actgggccga ggtcggaaag cagcttgagc tggaaggtgt 120

ggactccttc acagagagca ttgacangct actcgtgagc ctgcaggaga 170

<210>   512
<211>   169
<212>   DNA
<213>   Zea mays

<400>   512

ctcgatgggc tagaggcttc tggcttgagt gacttatccc gagttactag cgttgcatcc 60

ttctttgtca gccgagtgga cacccttatt gacaaaatgc ttgacaagat tggaacacct 120

gaggcccttg ccttgagagg aaaggctgca gtagcgcagg ccaaactag 169

<210>   513
<211>   259
<212>   DNA
<213>   Zea mays

<400>   513

gcgccttgga gaagcttggc attgactggg gcgaggtcgg aaagcagctt gagctggaag 60

gtgtggactc cttcaagaag acgcggtgac agcctactcg tgagcctaca ggagaagggc 120

aacagcctca agacggcaac tgtgtaaaac tgagaagatt gggtaccggc gggtgaacaa 180

cattactaaa taaaatgcta gcttgctggc tctcttagtt tttacgatgt acctttgctc 240

tccattttct gaatcgggga 259

<210>   514

172

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<211>      216
<212>      DNA
<213>      Zea mays

<223>      unsure at all n locations
<400>      514

ggaaagcagc ttgagctgga aggcgtggac tccttcaaga agagctttga cagcctactc    60

gtgagcctgc aggagaaggg caacagcctc aagatggcga gtgtgtaaag ctgagaagat   120

tgggtacctg cgagtgaacg attttactaa atanaatgct agcttgctgg ctctcctctt   180

agtttttacg ctgtactttg ctctcaattt tctgag                             216


<210>      515
<211>      291
<212>      DNA
<213>      Zea mays

<400>      515

catcgactgg gaagaggttg gaaagcagct tgagctggaa ggcgtggact ccttcaagaa    60

gagctttgac agcctactcg tgagcctgca ggagaagggc aacagcctca agatggcgag   120

tgtgtaaagc tgagaagatt gggtacctgc gagtgaacga ttttactaaa taaaatgcta   180

gcttgctggc tctcctctta gttttttacgc tgtacctttg ctctcaattt tctgagtcgg   240

ctttgtatcc cagcttgcca gaacgtcatg tgtagccatg ttcatggctg t            291


<210>      516
<211>      260
<212>      DNA
<213>      Zea mays

<400>      516

gcgtggactc cttcaagaag agctttgaca gcctactcgt gagcctgcag gagaagggca    60

acagcctcaa gatggcgagt gtgtaaagct gagaagattg ggtacctgcg agtgaacgat   120

tttactaaat aaaatgctag cttgctggct ctcctcttag ttttttacgct gtacctttgc   180

tctcaatttt ctgaatcggc tttgtatccc aggcttgcca gaacgtcatt gtgtagccac   240

tgttcatggc ttgtaattgc                                               260


<210>      517
<211>      327
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173

<212>   DNA
<213>   Zea mays

<400>   517

cgacggaaat agatgctcgg ttagcttatg acacccaggg cataatccac agggtacatg   60

aactgttgaa tctatacaac caacatgatg tctcaactga ccgcctgtta ttcaaaattc   120

ctgctacatg gcaaggcata gaggcctcaa ggttgcttga atctgaagga attcaaacgc   180

atctatcatt tgtttacagt ttcgcacaag cggcagcggc agcacaagct ggtgcatctg   240

tagtacaaat gtttgtgggc cgattgcggg actgggcagg catcactctg gtgacccaga   300

gatagatgaa gctttgaaga atggaga   327

<210>   518
<211>   203
<212>   DNA
<213>   Zea mays

<400>   518

cagggcataa tccacagggt acatgaactg ttgaatctat acaaccaaca tgatgtctca   60

actgaccgcc tgttattcaa aattcctgct acatggcaag gcatagaggc ctcaaggttg   120

cttgaatctg aaggaattca aacgcatcta catttgtttt acagtttcgc acaagcggca   180

gggtcagcac aagctggtgc atc   203

<210>   519
<211>   268
<212>   DNA
<213>   Zea mays

<400>   519

cctcaaggtt gcttgaatct gaaggaattc aaacgcatct aacatttgtt tacagtttcg   60

cacaagcgag cacggcagca caagctggtg catctgtagt acaaatgttt gtaggccgat   120

tgcgggactg ggcaaggcat cactctggtg acccagagat agatgaagct ttgaagaatg   180

gagaagatgc tgggctttct ttggcgaaga aagtatatgc ctatattcac aggaatgggt   240

acaaaacaaa gctgatggcc gctgccat   268

<210>   520
<211>   417

174

<212>   DNA
<213>   Zea mays

<400>   520

ggaacacctg aggcccttgc cttgagagga aaggctgcag tagcgcaggc cagactggca   60

aatcggctct ggcagaagaa attctctggc ccaaggtggg aggcgttggc caagaaaggt   120

gccaagaaac aaaggttgtt gtgggcatcc accggtgtca agaacccagc ttatcctgac   180

actctttatg tggacagtct catcggacct gacacggtca acacgatgcc cgaccaagct   240

ttgcaagcat tcatagacca cggcaccgtt tcaaggacag ttgatgcgaa tgtgtctgaa   300

gcggaaggtg tatacagcgc cttggagaag cttggcatcg actgggaaga ggttggaaag   360

cagcttgagc tggaaggcgt ggactccttc aagaagagct ttgacagcct actcgtg   417

<210>   521
<211>   424
<212>   DNA
<213>   Zea mays

<400>   521

aatcggctct accagaagaa attctctggc ccgaggtggg aggcgttggc caagaaaggt   60

gccatgaaac agaggttgtt gtgggcgttc accggtgtca agaacccagc ttatcccgac   120

actctttaca tcgactgtct cattggacct gacactgtca acacgatgcc cgaccaagct   180

ttgcaggcat tcatagacca cggcactgtt tcgaggacag ttgatgcgaa tgtgtacgag   240

gcggaaggtg tatacagcgc cttggacaat cttggcattg actggcgcga ggtcagaaag   300

cagcttgagc tggaaggtgt ggactccttc atgaagagct ttgacagcct actcgtgagc   360

ctgcaggaga tggtcaacat cctcaagacg gcatctgtgt aaaactgaga agattgtgta   420

ccgg   424

<210>   522
<211>   443
<212>   DNA
<213>   Zea mays

<400>   522

atttcggctg aaaggacgc ggagagcgct tactgggaac tcgttataaa ggatatccag   60

gatgcgtgca aactttttga gcccatctac gatgagactg atggggctga tgggtatgtc   120

175

tccgtagagg tgtctcctag gttggcaaat gacactcaag gaactgttga agcggcaaag   180

tggttacaca aagtggtcaa ccgcccaat gtctacataa agatcccagc tactgcagaa   240

tgtgttcctt ccatccagga agttatcgct aatggcatta gcgtcaacgt cacgcttatt   300

ttctcaattg caagatatga ggctgtgatt gatgcttacc tcgatgggct agaggcttct   360

ggcttgagtg acttatcccg agttactagc gttgcatcct tctttgtcag ccgagtggac   420

acccttattg acaaaatgct tga   443

<210>   523
<211>   438
<212>   DNA
<213>   Zea mays

<223>   unsure at all n locations
<400>   523

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gtccagcgca tatgatgagc agttcaagca gctcatttcg gcaggaaagg atgcggagag   120

cgcttactgg gaactcgtta taaaggatat ccaagatgcg tgcaaacttt ttgagcccat   180

ctacgacgag actgatgggg ctgatgggta tgtctccgta gaggtgtctc ctaggttggc   240

aaatgacact caaggaactg ttgaagcggc aaagtggtta cacaaagtgg tcaaccgccc   300

caatgtctac ataaagatcc cagctactgc agaatgtgtt ccttccatcc aggaagttat   360

cgctaatggc attagcgtca acgtcacgct tatnntctca attgcgagat atgaggctgt   420

gattgatgct tacctcga   438

<210>   524
<211>   369
<212>   DNA
<213>   Zea mays

<400>   524

gcgagatacg aggctgtgat tgatgcttac cttgatgggc tagaggctgg tggcttgagc   60

gacttatctt gagttaccag cgtcgcatgc ttctttgtca gtcgagtcta caccettatc   120

gacaaaatgc ttgagaagat tggaacacct gaggcacttg ccttgagagg gaaggctgcc   180

gacgtacagg ccaaactagc aaatcggctc taccagaaga aattctctgg cccgaggtgg   240

176

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gaagcgtctg ccaagaaagg tgccaagaaa cagatgttgt tgcgggcgtt cacccgtgtc   300

aagaacccag cttatcccga cactctttac atcgacagtc ttattggacc tgacacggtc   360

aacacgatt                                                            369


<210>      525
<211>      375
<212>      DNA
<213>      Zea mays

<400>      525

tgcttacctc gatgggctag aggcttctgg cttgagtgac ttatcccgag ttactagcgt    60

tgcgtccttc tttgtcagcc gagtggacac ccttattgac aaaatgcttg acaagattgg   120

aacacctgag gcccttgcct tgagaggaaa ggctgcagta gcacaggcca aactagcaaa   180

tcggctctac cagaagaaat tctctggccc aaggtgggag gcgttggcca agaaaggtgc   240

caagaaacaa aggttgttgt gggcatccac cggtgtcaag aacccagctt atcctgacac   300

tctggatgtg gacagtctca tctgacctga cacgttcaac acgatgcccg accaagcttt   360

gcaagcattt catag                                                     375


<210>      526
<211>      389
<212>      DNA
<213>      Zea mays                       .

<400>      526

cccacgcgtc cgctgcgctt catgatctct acgagctcca gggcctgtcc ccgtggtacg    60

agaacctatg ccgccctgtc acagacttgc tgcccattat cgccagcggc gtccgtggag   120

tcaccagcaa cccaacgatt ttccaaaagg ccatttcatc gtccagcgca tatgatgatc   180

agttcaagca gctcatttcg gcaggaaagg atgcggagag cgcttactgg gaactcgtta   240

taaaggatat ccaagatgcg tgcaaacttt ttgagcccat ctacgacgag actgatgggg   300

ctgatgggta tgtctccgta gaggtgtctc ctaggttggc aaatgacact caaggaactg   360

ttgaagcggc aaagtggtta cacaaagtg                                      389


<210>      527
<211>      379
<212>      DNA
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177

<213>   Zea mays

<223>   unsure at all n locations
<400>   527

aatcggctct accagaagaa attctctggc ccgaggtggg aggcgttggc cgagaagggt   60

gccatgaaac agaggttgtt gtgggcgtcc accggtgtca agaacccagc ttatcccgac   120

actctctaca tcgacagcct cattggacct gacacggtca acactatgcc cgtacaagct   180

ttgcatgcat tcatagacca cggcactgtt tcgaggacag ttgatgctaa tgtgtacgag   240

gcggaaggtg tatacagcgc cttggagaag cttggcattg actgnggcga ggtcggaaag   300

caacttgagc tggaaggtgt ggactccttc aagaagagct ttgacagcct actcgtgagc   360

ctgcatgaga agggcaaca   379

<210>   528
<211>   185
<212>   DNA
<213>   Zea mays

<400>   528

aggcctgtcc ccgtggtacg acaacctatg ccgccctgtc acagacttgc tgcccattat   60

cgccagcggc gtccgtggag tcaccagcaa cccaacgatt ttccaaaagg ccatttcatc   120

gtccagcgca tatgatgatc agttcaagca gctcatttcg gcaggaaagg atgcggagag   180

cgcta   185

<210>   529
<211>   374
<212>   DNA
<213>   Zea mays

<400>   529

gaggtacgcg tacgcgaaca cgatgcccga ccaagctttt caagcattca tagaccactg   60

caccgtttca aggacagttg atgcgaatgt gtctgaggcg gaaggtgtat acagcgcctt   120

ggagaagctt ggcatcgact gggaacaggt tggaaagcag cttgagctgg aacgcgtgga   180

ctccttcaag aagagctttg acagcctact cgtgagcctg caggacaagg gcaacagtct   240

caagatggcg agtgtgtaaa gctgataaga ttgggtacct gccagtgaac gattttacta   300

aataaaatgc tagcttgctg gctcttctct tactatttac gctgtacctt tgctctcaat   360

178

tatctgaatc ggct   374

<210>   530
<211>   348
<212>   DNA
<213>   Zea mays

<400>   530

gtctcaactg accgcctgtt attcataatt cctgctacat ggcaaggcat agaggcctca   60

aggttgcttg aatctgaagg aattcaaacg catctaacat ttgtttacag tttcgcacta   120

aagcggcagc ggcagcacaa gctggtgcat ctgtagtaca aatgtttgtg ggccgattgc   180

gggactgggc aaggcatcac tctggtgacc cagagataga tgaagctttg aagaatggag   240

aagatgctgg gctttctttg gcgaagaaag tatatgccta tattcacagg aatgggtaca   300

aaacaaagct gatggccgct gccataccga acaagcagga cgtattta   348

<210>   531
<211>   525
<212>   DNA
<213>   Zea mays

<223>   unsure at all n locations
<400>   531

gggggggtggg gttgactgtc atgttcgcgt ggcggtacaa agtcgaaatt gnccgggcca   60

cccacgcaac cgcatcgcga ccgccaaagc ccgcgacttt cagcctacgg aggccacatc   120

tggccgcgcg ggccgccgct ggcaacgcac ccacgtcccc ggtccgcgag gtcgtcactg   180

agctcgacgc ggtcgccggc ttcagcgaga tcgtgccgga caccgtcgtg ttcgatgatt   240

tcgagaggtt cgcacccacg gcggccacag tgagctcgtc gctgctgctt gggatcactg   300

ggctcccaga cactaagttc aagagtgcga tagatactgc actggcagat ggtgagtgca   360

acgcactgga gaaggctgat gacatgatgt cctgttacct caccaaggct cttgcatatg   420

ttggcgctga actggctcat caagtccctg ggagagtttc gacggaaata gatgctcggt   480

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<210>   532
<211>   423
<212>   DNA

179

<213>   Zea mays

<223>   unsure at all n locations
<400>   532

agagcctcca aaacctcgca acaaccccgt gacacccaca cccatccgcc ctgcgcctcc   60

tcgcgctccc caccaacccc gacgagcggc gatgaccggc acggtgtcca agctggcggc   120

gccccggcct gcggcgccac cgctccggcc ggcgtccctc cgcgccgccg caatcgcctt   180

cgcccctcc ccgcgccggg tccgcgtctc cgtcgccggg cgggccagga tccctccgt   240

cattgcgatg gcttctgcca aggaaggaaa tggtgcaccg accaagaaaa cctcgcttca   300

cgatctctac gagctccagg gcctctcccc gtggtatgac aacctctgcc gacctgtcac   360

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agctggcggc gccccggcct gcggcgccac cgctccggcc ggcgtccctc cgcgccgccg   180

caatcgcctt cgcccctcc ccgcgccggg tccgcgtctc cgtcgccggg cgggccagga   240

tccctccgt cattgcgatg gcttctgcca aggaaggaaa tggtgcaccg accaagaaaa   300

cctcgcttca cgatctctac gagctccagg gcctctcccc gtggtatgac aacctctgcc   360

gacctgtcac cgacttgctt gcccttatcg gcagcggtgt tcgtggagtc accagcaacc   420

ctacaattt   429

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<211>   283
<212>   DNA
<213>   Glycine max

<223>   unsure at all n locations
<400>   534

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ctgattctga gtgttatgga cttgaaaatc ctaacgcgcg attgtcttgt tttgtcaaca   120

aggctttcgc gaatatcggt agtgacatgg caaagcttgt ccctggccgt gtttcgacag   180

aagtggatgc gcggcttgct tatgacacac atgccattat caggaaggtg catgacctgt   240

tgaagttgta catgatannt atgtacctcc gcaacgtctg ttg                     283


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<400>        535

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acgtgggaag gtaactgttt attgttttcc aaactaattt ctattcttgg ctttggattt   120

attcactttt caaatgtcaa atatgctctt cggattgcat attgaatttt acaggcagca   180

gtagcccaag cagcattggc ttaccagctc taccaaagga aattttctgg tcaaagtggg   240

aactctaagt                                                          250


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<212>        DNA
<213>        Glycine max

<223>        unsure at all n locations
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ttgcttccat ttattgccaa tgggatcaga ggtgtcacta ccaacccagc ggtactcact   180

actcagtttt ttcttcacct gaaaacatta ctcttctcca tttggtttta tttttatcta   240

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gctatttcat cctcaaatgc ctacgatgat cag                                333


<210>        537
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<212>        DNA
<213>        Glycine max
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<400>   537

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cgggaaggca gcggtagccc aagcagcatt ggcttaccag ctctaccaaa ggaaattttc   120

tggtccaagg tgggaagctc tagttaaaaa gggggccaag aagcaaaggc tcctctgggc   180

ctcaaccagt gtaaagaatc ctgcctattc tgacacctta tatgttgctc ctcttattgg   240

acccgacact gtatcaacaa tgccagacca agcccttcaa   280

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<211>   294
<212>   DNA
<213>   Glycine max

<223>   unsure at all n locations
<400>   538

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gcttaccacc tctaccaaag gaaattttct ggtccaaggt gggaagctct agttaaaaag   180

ggggccaaga agcaaaggct ctttgggcct caaccagtgt aaagaaccct gcctattctg   240

acacntatat gttgctcctc tattggaccc gacatgatca accagccaga ccaa   294

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<211>   221
<212>   DNA
<213>   Glycine max

<223>   unsure at all n locations
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atctacgcgg gaaggcagcg gtagcccaag cagcattggc ttaccagctc taccaaagga   120

aattttctgg tccaaggtgg gaagctctag ttaaaaaggg ggccaagaag caaaggctcc   180

tctgggcctc aaccagtgta aagaatcctg cctattctga c   221

<210>   540
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<212>   DNA
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182

<400>   540

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tcgccctgtt tcaggtttgc ttccatttat tgccaatggg atcagaggtg tcactaccaa   180

cccagcgatt tttgaaagag ctatttcatc ctcaaatgcc tacgatgatc agttgaggga   240

attggtaggg gcagggaagg acatagaaag tgcttattgg gaattggttg tgaaggaca   299

<210>   541
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<212>   DNA
<213>   Glycine max

<400>   541

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atttattgcc aatgggatca gaggtgtcac taccaaccca gcgatttttg aaagagctat   120

ttcatcctca aaatgctacg atgatcagtt gagggaaatg gtcagggcca ggaaggacat   180

agaaagtgct tattgggaat tggttgtgaa ggacatacag gatacttgca acttctgga   240

<210>   542
<211>   278
<212>   DNA
<213>   Glycine max

<223>   unsure at all n locations
<400>   542

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tctattctca gtttgcggtg tttgatagaa ataatggatc ggaaccggcc aaagatcaaa   120

agtacaattc ttcaccatct ctatgagaag cagagacaga gcccttacta tgacaatctc   180

tgtcgccctg tttcagattt gcttccattt attgccaatg ggatcagagg tgtcactacc   240

aacccagcga tttttganag agctatttca tcctcaag   278

<210>   543
<211>   254
<212>   DNA
<213>   Glycine max

183

<400>   543

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aaataatgga tcggaacggg ccaaagatca aaagtacaat tcttcaccat ctctatgaga   120

agcagagaca gagcccttac atgacaatct ctgtcgccct gtttcagatt tgcttccatt   180

tattgccaat gggatcagag gtgtcactac caacccagcg atttttgaaa gagctatttc   240

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<212>   DNA
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<400>   544

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cttatatgtt gctcctctta ttggacccga cactgtatca accatgccag accaagccct   120

tcaagcattt attgatcatg gtaccgtatc caggacaata gactcaaatg catctgaagc   180

tgaaggaata tacaatgctc tccagaaatt gggtattgac tggagctttg ttggtt   236

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<400>   545

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ctcctcttat tggacccgac actgtatcaa ccatgccaga ccaagccctt caagcattta   120

ttgatcatgg taccgtatcc aggacaatag actcaatgca tctgaagctg aaggaatata   180

caatgctctc cagaaattgg gtattgactg gagctttgtt ggttcccagc ttgaacttga   240

aggagtggac tcgtttaaga   260

<210>   546
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<213>   Glycine max

<400>   546

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cttgaacttg aaggagtgga ctcgtttaag aagagctttg acagcctcct ggattctctg   120

caagagaagg caaactctct taagttggtc agccattgaa gtgtgaacgt catagttagt   180

aatgcagtgc tatgtatgaa gtgatttatg gattaataaa aggcagtggc tgtgcatttt   240

gtgctgctgt   250

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ctcccagctt gaacttgaag gagtggactc gtttaagaag agctttgaca gcctcctgga   120

ttctctgcaa gagaaggcaa actctcttaa gttggtcagc cactgaagtt tgaacgtcat   180

ggttagtaat gcagtgctgt gtatgatggc atctatggat taataaaagg cagcggctgt   240

gcatttgtg ctgctgcaaa tgtgc   265

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<212>   DNA
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<400>   548

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agtcatttat ttagacgata gtgatacaat gtaaatggga aaaattgtcc gcttcaagtc   180

aagcgttttg ttttttcccc actatacaat ggttgtgcgt ttatgttt   228

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<212>   DNA
<213>   Glycine max

<400>   549

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185

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agtcatttat ttagacgata gtgatacaat gtacttggga aaaattgtcc gcttcaagtc   180

aagcgttttg ttttttcccc actatacaat ggttgtgcga ttat   224

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<211>   238
<212>   DNA
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tctttatgag aaagaagggc agagtccatg gtatgataat ctctgcagac ctgttacaga   120

ccttcttcct cttatagcaa gtggtgtcag aggcgtcact agcaaccctg cgattttca   180

gaaagctatc tcatcatcga atgcttacaa tgatcagttc agggaacttg tgcaagca   238

<210>   551
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<212>   DNA
<213>   Glycine max

<400>   551

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gtccatggta tgataatctc tgcagacctg ttacagacct gcttcctctt atagcaagtg   120

gtgtcagagg cgtcactagc aaccctgcga tctttcagaa agctatctca tcatcgaatg   180

cttacaatga tcagttcagg gaacttgtgc aaacagggaa agacattgaa agtgcatatt   240

gggaacttgt agtgaaggat atccaagat   269

<210>   552
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<212>   DNA
<213>   Glycine max

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gatcaaatgc tcccaaacag atgggaatgg aagtcctgca agaggacag tgcttcatga   120

tctttatgag aaagaagggc agagtccatg gtatgataat ctctgcagac ctgttacaga   180

186

ccttcttcct cttatagcaa gtggtgtcag aggcgtcact agcaaccctg cgatttttca 240

gaaagctatc tcatcatcga atgcttacaa tg   272

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<213>   Glycine max

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tgcaaagagg acagtgcttc atgatcttta tgagaaagaa gggcagagtc catggtatga 120

taatctctgc agacctgtta cagacctgct tcctcttata gcaagtggtg tcagaggcgt 180

cactagcaac cctgcgatct ttcagaaagc tatctcatca tcgaatgctt a   231

<210>   554
<211>   237
<212>   DNA
<213>   Glycine max

<223>   unsure at all n locations
<400>   554

tacaaaatta acctctccgc ttccaccnga tccattcact cactcnntct taaaanctcc   60

ttncggatca aatgctccca aacagatggg aatggaagtc ctgcaaagag gacagtgctt 120

catgatcttt atgagaaaga acngcagagt ccatggtatg ataatctctg cagacctgtt 180

acagaccttc ttcctcttat agcaagtggt gtcagaggng tcactagcaa ccctgng   237

<210>   555
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<212>   DNA
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acggatcaaa tgctcccaaa cagatgggaa tggaagtctg caaagaggac agtgcttcat 120

gatctttatg agaaagaagg gagagtccat ggtatgataa tctctgcaga cctgttacag 180

actgcttctc ttatagcaag tggtgtcaga ggcgtcatta gcaacctgcg catctttcag 240

aaagctatct catcatcgaa tgttacatga   270

187

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<212>       DNA
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gagattctcg cttcctctcc ttcaatcctt cttccaacgc tattaattac aaaattaacc  120

tctccgcttc cctccgatcc attcactccc tccctcttaa aacctccttg cggatcaaat  180

gctcccaaac agatgggaat ggaagtcctg caaagaggac agtgcttcat gatctttatg  240

agaaagaagg gcagagtcca tggtatgata atctctgcag acctgttaca ga           292


<210>       557
<211>       165
<212>       DNA
<213>       Glycine max

<400>       557

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gcggatcaaa tgctcccaaa cagatgggaa tggaagtcct gcaaagagga cagtgcttca  120

tgatctttat gagaaagaag ggcagagtcc atggtatgat aatct                  165


<210>       558
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<400>       558

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agattctcgc ttcctctcct tcaatccttc ttccaacgct attaattaca aaattaacct  120

ctccgcttcc ctccgatcca ttcactccct ccctcttaaa acctccttgc ggatcacctg  180

ctcccaaaca gatgggaatg gaagtcctgc aaagaggaca gtgcttcatg atctttatga  240

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<210>       559
<211>       275
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<212>       DNA
<213>       Glycine max

<223>       unsure at all n locations
<400>       559

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gagattctcg cttcctctcc ttcaatcctt cttccaacgc tattaattac aaaattaacc     120

tctccgcttc cctccgatcc attcactccc tccctcttaa aacctccttg cggatcaaat     180

gctcccaaac agatgggaat ggaagtcctg caaagaggac agtgcttcat gatctttatg     240

aganagaagg gcagagtcca tggtatgata atctc                               275


<210>       560
<211>       274
<212>       DNA
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<400>       560

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gattctcgct cctctccttt caatccttct tccaacgcta ttaattacaa aattaacctc     120

tccgcttccc tccgatccat tcactcctcc ctcttaaaac tccttgcgg atcaaatgct     180

cccaaacaga tgggaatgga agtcctgcaa agaggacagt gcttcatgat ctttatgaga     240

aagaagggca gagtccatgg tatgataatc tctg                                274


<210>       561
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<212>       DNA
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<400>       561

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gagattctcg cttcctctcc ttcaatcctt cttccaacgc tattaattac aaaattaacc     120

tctccgcttc cctccgatca ttcactccct ccctcttaaa acctccttgc ggatcaaatg     180

ctcccaaaca gatgggaatg gaagtcctgc aaagaggaca gtgcttcatg atctttatga     240

gaaagaaggg cagagtccat ggtatgataa                                     270


<210>       562
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<211>   265
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<213>   Glycine max

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ccccagagat tctcgcttcc tctccttcaa tccttcttcc aacgctatta attacaaaat   120

taacctctcc gcttccctcc gatccattca ctccctccct cttaaaacct ccttgcggat   180

caaatgctcc caaacagatg ggaatggaag tcctgcaaag aggacagtgc ttcatgatct   240

ttatgagaaa gaagggcaga gtcca   265

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<211>   261
<212>   DNA
<213>   Glycine max

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gattctcgct cctctccttt caatccttct tccaacgcta ttaattacaa aattaacctc   120

tccgcttccc tccgatccat tcactccctc cctcttaaaa cctccttgcg gatcaaatgc   180

tcccaaacag atgggaatgg aagtcctgca agaggacag tgcttcatga tctttatgag   240

aaagaagggc agagtccatg g   261

<210>   564
<211>   282
<212>   DNA
<213>   Glycine max

<400>   564

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agagattctc gcttcctctc cttcaatcct tcttccaacg ctattaatta cacaattaac   120

ctctccgctt ccctccgatc cattcactcc ctccctctta aaacctcctt gcggatcaaa   180

tgctcccaaa cagatgggaa tggaagtcct gcaaagagga cagtgcttca tgatctttat   240

gagaaagaag gcagagtcc atggtatgat aatctctgca ga   282

<210>   565

190

<211>   290
<212>   DNA
<213>   Glycine max

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tccacttgct tccttatcag aagcgcttcg cccccgagat tctcgcttcc tcaccttcaa   120

accttcttcc atcgctttta atcacaaaac taacctatcc gcttccctcc gatccattca   180

ctcgctccct cttaaaacct ccttacggat caaatgctcc caaacagatg ggaatggaag   240

tcctgcaaag aggacagtgc ttcatgatct ttatgagaaa gaagggcaga   290

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<211>   256
<212>   DNA
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<400>   566

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gagattctcg cttcctctcc ttcaatcctt cttccaacgc tattaattac aaaattaacc   120

tctccgcttc cctccgatcc attcactccc tccctcttaa aacctccttg cggatcaaat   180

gctcccaaac agatgggaat ggaagtcctg caaagaggac agtgcttcat gatctttatg   240

agaaagaagg gcagag   256

<210>   567
<211>   271
<212>   DNA
<213>   Glycine max

<400>   567

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acttgcttcc ttatcagaag cgcttcgccc ccgagattct cgcttcctca ccttcaaacc   120

ttcttccatc gcttttaatc acaaaactaa cctatccgct tccctccgat ccattcactc   180

gctccctctt aaaacctcct tacggatcaa atgctcccaa acagatggga atggaagtcc   240

tgcaaagagg acagtgcttc atgatcttta t   271

<210>   568

<211>   284
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ctgcttcctt atcagaagcg cttcgcccca gagattctcg cttcctctcc ttcaatcctt   120

cttccaacgc tattaattac aaaattaacc tctccgcttc cctccgatcc attcactccc   180

tccctcttaa aacctccttg cggatcaaat gctcccaaac agatgggaat ggaagtcctg   240

caaagaggac agtgcttcat gatctttatg agaaagaagg gcag   284

<210>   569
<211>   264
<212>   DNA
<213>   Glycine max

<400>   569

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cttccttatc agaagcgctt cgcccccgag attctcgctt cctcaccttc aaaccttctt   120

ccatcgcttt taatcacaaa actaacctat ccgcttccct ccgatccatt cactcgctcc   180

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agaggacatg cttcatgatc ttta   264

<210>   570
<211>   250
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<213>   Glycine max

<400>   570

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ttcgccccag agattctcgc ttcctctcct tcaatccttc ttccaacgct attaattaca   120

aaattaacct ctccgcttcc ctccgatcca ttcactccct ccctcttaaa acctccttgc   180

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atctttatga   250

<210>   571

192

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cttccttatc agaagcgctt cgcccccgag attctcgctt cctcaccttc aaacctactc   120

ccatcgcttt taatcacaaa actaacctat ccgcttccct ccgatccatt cactcgctcc   180

ctcttaaaac ctccttacgg atcaaatgct cccaaacaga tgggaatgga agtcctgcaa   240

cgaggacagt gcttcatgat ctttatgaga aa   272

cgcttcgtga cttgcagcaa ttcccaatgg cttccgtttc caagctctca acgccaaatc   60

cacttgcttc cttatcagaa gcgcttcgcc cccgagattc tcgcttcctc accttcaaac   120

cttcttccat cgcttttaat cacaaaacta acctatccgc ttccctccga tccattcact   180

cgctccctct aaaacctcc ttacggatca aatgctccca aacagatggg aatggaagtc   240

ctgcaaagag gacagtgctt catgatcttt at   272

ctcaacgcca tctccagctg cttccttatc agaagcgctt cgccccagag attctcgctt   60

cctctccttc aatccttctt ccaacgctat taattacaaa attaacctct ccgcttccct   120

ccgatccatt cactccctcc ctcttaaaac ctccttgcgg atcaaatgct cccaaacaga   180

tgggaatgga agtcctgcaa agaggacagt gcttcatgat ctttatgaga aagaagg   237

193

<213>   Glycine max

<400>   574

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tctccgcttc cctccgatcc attcactccc tccctcttaa aacctccttg cggatcaaat   180

gctcccaaac agatgggaat ggaagtcctg caaagaggac agtgcttcat gatctttatg   240

agaaagaagg g   251

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cttccttatc agaagcgctt cgcccccgag attctcgctt cctcaccttc aaaccttact   120

ccatcgcttt taatcacaaa actaacctat ccgcttccct ccgatccatt cactcgctcc   180

ctcttaaaac ctccttacgg atcaaatgct cccaaacaga tgggaatgga agt   233

<210>   576
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<212>   DNA
<213>   Glycine max

<400>   576

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gagattctcg cttcctctcc ttcaatcctt cttccaacgc tattaattac aaaattaacc   120

tctccgcttc cctccgatcc attcactccc tccctcttaa aacctccttg cggatcaaat   180

gctcccaaac agatgggaat ggaagtcctg caaagaggac agtgcttcat gatctttatg   240

agaaagacgg gcagagtcca tggtatgatc atctctgca   279

<210>   577
<211>   244
<212>   DNA
<213>   Glycine max

194

<400> 577

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gagattctcg cttcctctcc ttcaatcctt cttccaacgc tattaattac aaaattaacc   120

tctccgcttc ctccgatcca ttcactccct ccctcttaaa acctccttgc ggatcaaatg   180

ctcccaaaca gatgggaatg gaagtcctgc aaagaggaca gtgcttcatg atctttatga   240

gaaa   244

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<400>   578

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tcgcttcctc tccttcaatc cttcttccaa cgctattaat tacaaaatta acctctccgc   120

ttccctccga tccattcact ccctccctct aaaacctcc ttgcggatca aatgctccca   180

aacagatggg aatggaagtc ctgcaaagag gacagtgctt catgatcttt atgagaaaga   240

gggcagagt   249

<210>   579
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<212>   DNA
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<400>   579

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gagattctcg cttcctctcc ttcaatcctt cttccaacgc tattaattac aaaattaacc   120

tctccgcttc cctccgatcc attcactccc tccctcttaa aacctccttg cggatcaaat   180

gctcccaaac agatgggaat ggaagtcctg caaagaggac agtgcttcat gatctttatg   240

agaaa   245

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<212>   DNA
<213>   Glycine max

195

<400>   580

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tttgaaccaa tctatgatca aacagatggt ggtgatggta tgtttctgtt gaagtatctc   180

ctaggctcgc tgatgacact gagggaacca tagaagctgc aaaatggctt cataaagtgg   240

ttgatcgccc caatgtgtat attaagattc ctgctacaga ggcatgtgtg cct   293

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<211>   271
<212>   DNA
<213>   Glycine max

<223>   unsure at all n locations
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tcagaaagct atctcatcat cgaatgctta caatgatcag ttcagggaac ttgtgcaaac   120

agggaaagac attgaaagtg catattggga acttgtagtg aaggatatcc aagatgcttg   180

cagactattt gaaccaatct atgatcaaac agatggtggt gatgggtatg tttctgtnga   240

agtatctcct aggctcgctg atgacactga g   271

<210>   582
<211>   274
<212>   DNA
<213>   Glycine max

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gtttctgttg aagtatctcc caggctcgct gatgacactg agggaaccat agaagctgca   120

aaatggcttc ataaagtggt tgatcgcccc aatgtgtata ttaagattcc tgctacagag   180

gcatgtgtgc cttcaattaa ggaagttatt gctaatggga taagtgtgaa tgtgacgctg   240

atattctctc ttgcaagata tgaagctgta atag   274

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<212>   DNA
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196

<400> 583

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ctcccaggct cgctgatgac actgagggaa ccatagaagc tgcaaaatgg cttcataaag 180

tggttgatcg ccccaatgtg tatattaaga ttcctgctac agaggcatgt gtgccttcaa 240

ttaaggacgt tattgctaat gggataa 267

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<212>   DNA
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<400>   584

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accaatctat gatcaaacag atggtggtga tgggtatgtt tctgttgaag tatctcctag 120

gctcgctgat gacactgagg gaaccataga agctgcaaaa tggcttcata aagtggttga 180

tcgccccaat gtgtatatta agattcctgc tacagaggca tgtgtgcctt caattaagga 240

agttattg 248

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<211>   253
<212>   DNA
<213>   Glycine max

<400>   585

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gatgcttgca aattatttga accaatctat gatcaaacag atggtggtga tggctatgtt 180

tctgttgaag tatctcccag gctcgctgat gaacctgagg gaaccatagc agctgcaaaa 240

tggcttcata aag 253

<210>   586
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<212>   DNA
<213>   Glycine max

197

<400>   586

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gtgacgctga tattctctct tgcaagatat gaagctgtaa ttgatgcata cttggatggt   180

cttgaggcat ctgagttaaa tgacctctct agagttacaa gtgttgcctc tttcttcgtc   240

agtagagtgg aca   253

<210>   587
<211>   264
<212>   DNA
<213>   Glycine max

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ttgaagtatc tcctaggctc gctgatgaca ctgagggaac cattgaagct gcaaaatggc   180

ttcataaagg gttgatcgcc ccaatgtgta tattaagatt cctgctacag aggcatgtgt   240

gccttcaatt aaggaagtta ttgc   264

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<212>   DNA
<213>   Glycine max

<400>   588

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gcatctgggt taaatgacct ctctagagtt acaagtgttg cctctttctt tgtcagtaga   120

gtggacactc tcattgaaag gcccttgaga aaattggcac cccagaggct cttaatctac   180

gtgggaaggc agcagtagcc caagcagcat tggcttacca gctctaccaa aggaaatttt   240

ctggtccaag gtgggaagct cta   263

<210>   589
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<212>   DNA
<213>   Glycine max

198

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gcctctttct ttgtcagtag agtggacact ctcattgaca aggcccttga gaaaattggc　　180

accccagagg ctcttaatct acgtgggaag gcagcagtag cccaagcagc attggcttac　　240

cagc　　　　　　　　　　　　　　　　　　　　　　　　　　244

<210>　　590
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<212>　　DNA
<213>　　Glycine max

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tgggaacttg tagtgaagga tatccaagat gcttgcagac tatttgaacc aatctatgat　　120

caaacagatg gtggtgatgg gtatgtttct gttgaagtat ctcctaggct cgctgatgac　　180

actgagggaa ccatagaagc tgcaaaatgg cttcataaag tggttgat　　　　228

<210>　　591
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gaatgtgacg ctgatattct ctcttgcaag atatgaagct gtaatagatg cttacttgga　　180

tggtcttgag gcatctgggt taaatgacct ctctagagtt acaagtgttg cctctcactt　　240

tgtcagtaga gtggacactc tcatt　　　　　　　　　　　265

<210>　　592
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<212>　　DNA
<213>　　Glycine max

<400>　　592

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aacagggaaa gacattgaaa gtacatattg ggaacttgta gtgaaggata tccaagatgc   120

ttgcagacta tttgaaccaa tctatgatca aacagatggt ggtgatgggt atgtttctgt   180

tgaagtatct cctaggctcg ctgatgacac tgagggaacc atagaagctg caaaatggct   240

tcataaagtg gttgatcgcc ccaatgtgta tattaagatt c                       281
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<210>   593
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<212>   DNA
<213>   Glycine max

<223>   unsure at all n locations
<400>   593

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aaagtgcata ttgggaactt gtagtgaagg atatcnaaaa tgcnaaaaan gananttgaa   120

accaatctat gancaaacag atggnggtga tgggtatgtt tctgttgaag tatctcctag   180

ggctcgctga tgaacactga gggaaccata gaagctgcaa aatggcttca taaagtggnt   240

gatcggccca atgtgtatat taagattcct gnttacagag g                       281
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<210>   594
<211>   260
<212>   DNA
<213>   Glycine max

<400>   594

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tcttgcaaga tatgacgctg taatagatgc ttacttggat ggtcttgagg catctgggtt   120

aaatgacctc tctagagtta caagtgttgc ctctttcttt gtcagtagag tggacactct   180

cattgacaag gcccttgaga aaattggcac cccagaggct cttaatctac gtgggaaggc   240

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<210>   595
<211>   217
<212>   DNA
<213>   Glycine max

200
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<400>    595

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gaagctgtaa ttgatgcata cttggatggt cttgaggcat ctgagttaaa tgacctctct   120

agagttacaa gtgttgcctc tttcttcgtc agtagagtgg acaccctcat tgacaaggcc   180

cttgagaaaa ttggcacccc agtggccctt aatctac                            217


<210>    596
<211>    212
<212>    DNA
<213>    Glycine max

<400>    596

ctatgatcaa acagatggtg ctgatggcta tgtttctgtt gaactatctc ccaggctcgc    60

tgatgacact gagggaacca tagaagctgc aaaatggctt cataaagtgg ttgatcgccc   120

caatgtgtat attaagattc ctgctacaga ggcatgtgtg ccttcaatta aggaagttat   180

tgctaatggg ataagtgtga atgtgacgct ga                                 212


<210>    597
<211>    289
<212>    DNA
<213>    Glycine max

<223>    unsure at all n locations
<400>    597

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cgcatcatcg aaggnttacn atgatcngtt cagggaactt ggtgcaagca gggaaagaca   120

ttgaaagtgc atattgggaa ctngtagtga aggatatcca agatgcttgc aaattatttg   180

aaccantcta tnatcaaaca gatggtggtg atggctatgt ttctgttgaa gtatctccca   240

ggctcgctga tgacactgag gganccatag aactgcaaaa tggcttcat               289


<210>    598
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<213>    Glycine max

<400>    598

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201

gatggtcttg aggcatctga gttaaatgac ctctctagag ttacaagtgt tgcctctttc    120

ttcgtcagta gagtggacac cctcattgac aaggcccttg agaaaattgg cacccccagtg   180

gcccttaatc tacgcgggaa ggcagcggta gcccaagcag cattggctta ccagctctac    240

caaaggaaat tttctggtcc                                                 260


<210>        599
<211>        229
<212>        DNA
<213>        Glycine max

<400>        599

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atatgaagct gtaattgatg catacttgga tggtcttgag gcatctgagt taaatgacct    120

ctctagagtt acaagtgttg cctctttctt cgtcagtaga gtggacaccc tcattgacaa    180

ggcccttgag gaaattggca ccccagtggc ccttaatcta cgcgggaag                229


<210>        600
<211>        182
<212>        DNA
<213>        Glycine max

<400>        600

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ctggatggtc ttgaggcatc tgagttaaat gacctctcta gagttacaag tgttgcctct    120

ttcttcgtca gtagagtgga caccctcatt gacaaggccc ttgagaaaat tggcaccccca   180

gt                                                                    182


<210>        601
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<212>        DNA
<213>        Glycine max

<400>        601

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ctcatattct gcctccctaa atatgaagca gtgattgatg cttacttgga tggccttgag    120

tcttgtggca tgactgatct ctctaaggtt tcaagtgcag cagcattcta catcagtaga    180


202

gtggatgtta cacttgacaa gaaacttgag caaattggta ctactgaggc tcttgatctc    240

aaaggaaagg gtgcggttgc tcaagcagtc ttagcatacc aactttacca gaaaaaattt    300

tctggtccaa gatgggaacg cttggagaat agaagtgcca agaagcagag gttgatgtgg    360

gcttcaacaa atgtgaaaaa tccatcttac cctgacaca                           399


<210>          602
<211>          405
<212>          DNA
<213>          Glycine max

<223>          unsure at all n locations
<400>          602

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tcagtagaat ggacaccctc attgacaagg cccttgagaa aattggcacc ccaatggccc    120

ttaatctacg tgggaaggca acggtagccc aagcagcatt ggcttaacag ctctaccaaa    180

gaaattttct ggtccaaagt gggaagctct agttaaaaag ggggccaaga agcaaaggct    240

cctctgggcc ttaaccagtg taaagaatcc tgcctattct gacaccttat atgttgctcc    300

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<210>          603
<211>          399
<212>          DNA
<213>          Glycine max

<400>          603

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cccttactat gacaatctct gtcgccctgt ttcagatttg cttccattta ttgccaatgg    120

gatcagaggt gtcactacca acccagcgat tttttgaaaga gctatttcat cctcaaatgc    180

ctacgatgat cagttgaggg aattggtagg ggcagggaag gacatagaaa gtgcttattg    240

ggaattggtt gtgaaggaca tacaggatac ttgcaaactt ctggagccaa tttacaatga    300

aacagatggg gaagatggac atgtatctct tgcagtttcc ccaaagctag caaatgacac    360

caaggggaca attgaggcag caaaatggct tcataatat                           399


203

<210> 604
<211> 418
<212> DNA
<213> Glycine max

<223> unsure at all n locations
<400> 604

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tcaaatgcat ctgaagctga aggaatatac aatgctctcc agaaattggg tattgactgg   120

agctttgttg gttcccagct tgaacttgaa ggagtggact cgtttaagaa gagctttgac   180

agcctcctgg attctctgca agagaaggca aactctctta agttggtcag ccactgaagt   240

ttgaacgtca tggttagtaa tgcagtgctg tgtatgatgg catctatgga ttaataaaag   300

gcagcggctg tgcattttgt gctgctgcan atgtgcttca tggagtcatt tatttagacg   360

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<210> 605
<211> 396
<212> DNA
<213> Glycine max

<400> 605

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tcactccctc cctcttaaaa cctccttgcg gatcaaatgc tccaaacaga tgggaatgaa   180

gtcctgcaaa gaggacagtg cttcatgatc tttatgagaa agaagggcag agtccatggt   240

atgataatct ctgcagacct gttacagacc ttcttcctct tatagcaagt ggtgtcagag   300

gcgtcactag caaccctgcg atttttcaga aagctatctc atcatcgaat gcttacaatg   360

atcagttcag ggaacttgtg caagcaggga aagaca                            396
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<210> 606
<211> 428
<212> DNA
<213> Glycine max

<400> 606

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204

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tctccgcttc cctccgatcc attcactccc tccctcttaa aacctccttg cggatcaaat 180

gctcccaaac agatgggaat ggaagtcctg caaagaggac agtgcttcat gatctttatg 240

agaaagatag gcagagtcca tggtatgata atctctgcag acctgttaca gaccttctta 300

ctcttatagc aagtggtgtc agaggcgtca ctagcaaccc tgcgattttt cagaaagcta 360

tctcatcatc gaatgcttac aatgatcagt tcaaggaact tgtgcaagca tggaaagaca 420

ttgaaagt   428

<210>   607
<211>   373
<212>   DNA
<213>   Glycine max

<400>   607

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ctgcttcaat ccttatgcca acgctatcaa ttacaaaatt gacctctccg cttgcctccg 120

atccattcac tccctgccta ttaaaaccta cttgcggatc aaatgctccc aaacagatgg 180

gaatggaagt cctgctaaga ggacagcgct tcatgatctt tatgagaaag aagggcagag 240

tccatggtat gataatctct gcagacctgt tacagagctt gttcctgtta tagcacgtgg 300

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ttacaatgat cag   373

<210>   608
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<212>   DNA
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<400>   608

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taattacaaa attaacctct ccgcttccct ccgatccatt cactccctcc ctcttaaaac 180

ctccttgcgg atcaaatgct cccaaacaga tgggaatgga agtcctgcaa agaggacagt 240

gcttcatgat ctttatgaga agaaaggca gagtccatgg tatgataatc tctgcagacc 300

205

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tgttacagac cttcttcctc ttatagcaag tggtgtcaga ggcgtcacta gcaaccctgc    360

gatttttcag aaagctatct catcatcgaa tgcttacaat gatca                     405


<210>        609
<211>        417
<212>        DNA
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<400>        609

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aatggcctcc attttcaagc tctcaacgcc atctccagct gcttccttat cagaagcgct    120

tcgccccaga gattctcgct tcctctcctt caatccttct tccaacgcta ttaattacaa    180

aattaacctc tccgcttccc tccgatccat tcactccctc cctcttaaaa cctccttgcg    240

gatcaaatgc tcccaaacag atgggaatgg aagtcctgca aagaggacag tgcttcatga    300

tctttatgag aaagaagggc agagtccatg gtatgataat ctctgcagac ctgttacaga    360

ccttcttcct cttatagcaa gtggtgtcag aggcgtcact agcaaccctg cgatttt       417


<210>        610
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<212>        DNA
<213>        Glycine max

<400>        610

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agaagacgac agaaggggac tccatcctcc gcttcgtgac ttgcagcaat tcccaatggc    120

ttccgtttcc aagctctcaa cgccaaatcc acttgcttcc ttatcagaag cgcttcgccc    180

ccgagattct cgcttcctca ccttcaaacc ttcttccatc gcttttaatc acaaaactaa    240

cctatccgct tccctccgat ccattcactc gctccctctt aaaacctcct tacggatcaa    300

atgctcccaa acagatggga atggaagtcc tgcaaagagg acagtgcttc atgatcttta    360

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206

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tctccgcttc cctccgatcc attcactccc tccctcttaa aacctccttg cggatcaaat   180

gctcccaaac agatgggaat ggaagtcctg caaagaggac agtgcttcat gatctttatg   240

agaaagaagg gcagagtcca tggtatgata atctctgcag acctgttaca gaccttcttc   300

ctcttatagc aagtggtgtc agaggcgtca ctagcaaccc tgcgattttt cagaaagcta   360

tctcatcatc gaatgcttac aatgatcagt tcacggaact tgtgcaagcg ggaaagacat   420

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aacctctccg cttccctccg atccattcac tccctccctc ttaaaacctc cttgcggatc   180

aaatgctccc aaacagatgg gaatggaagt cctgcaaaga ggacagtgct tcatgatctt   240

tatgagaaag aagggcagag tccatggtat gataatctct gcagacctgt tacagacctt   300

cttcctctta tagcaagtgg tgtcagaggc gtcactagca ccctgcgat ttttcagaaa    360

gctatctcat catcgaatgc ttacaatga                                     389
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cgatccattc actccctacc tcttaaaacc tacttgcgga tcaaatgctc ccaaacagat   180
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207

gggaatggaa gtcctgcaaa gaggacagtg cttcatgatc tttatgagaa agataggcag   240

aatccatgga atgacaatct ctgcaaacct gttacagacc ttcttcctct tatagcaagt   300

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gcaaaatggc ttcataaagt ggttgatcgc cccaatgtgt atattaagat tcctgctaca   180

gaggcatgtg tgccttcaat taaggaagtt attgctaatg ggataagtgt gaatgtgacg   240

ctgatattct ctcttgcaag atatgaagct gtaatagatg cttacttgga tggtcttgag   300

gcatctgggt taaatgacct ctctagagtt acaagtgttg cctctttctt tgtcagtaga   360

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208

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aatgacctct ctagagttac aagtgttgcc tctttctttg tcagtagagt ggacactctc   180

attgacaagg cccttgagaa aattggcacc ccagaggctc ttaatctacg tgggaaggca   240

gcagtggccc aagcagcatt ggcttaccag cgtctccgaa ggaaatgttc tggtccaagg   300

tgggaagctc tagttaaaaa tggggcca   328

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<212>   DNA
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209

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ggacgtattt agccttctgg ggattgatta cattattgcc cactgaagat            290


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<213>      Zea mays

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aactggcaac tactcttgta attgtcattt ctaagagcgg aggcacacct gaaacccgca   120

atggtctact agaagtacag aaagccttca gagatgcggg gctgcaattc tcgaaacagg   180

gtgttgcaat tactcaagaa aattctctgt tggataacac tgctagaata gagggatggt   240

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ccaagatgtc atctctggaa agattctttc cccatctggt cgtttcactt caattctctc   180

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actgggttgg tggtaggact tcagaaatgt cagctgttgg tttacttcca gctgcattgc   120

agtgtattga tatcaaggaa atgctatttg gtgcagcttt aatggatgag gaaacccgga   180
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210

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aggggggaact gctgaagc                                                 258


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acgaagcatt aaagatttgg atccagaaac cactctggtg gtggctgtat caaagacatt   120

cacaacagct gaaacaatgt taaatgctcg aactcctaag gagtggatcg tttcttctct   180

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ggaaacagct gcatggaacc cggatggaag gaaagcctgt tgagggtttt aaccacagca   180

cttcaagttt gcttgcacga tatcttgctg tcaagccatc cacccgtat gatactaccg   240


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aacactgcta gaatagaggg atggttagct cggtttccta tgtttgattg ggttggtggt  120

aggacttcag aaatgtctgc tgtgggttta cttccagctg cattgcaggg tattgatatc  180

aaggaaatgc tagctggtgc agctttaatg gatgaagaaa cccggaacac tgtggttaaa  240

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ttacttccag ctgcattgca gggtattgat atcaaggaaa tgctagttgg tgcagcttta  180

atggatgagg aaacccggaa cactgtggta tcacattatt aataacacgg acaacttgca  240

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ggataacact gccagaatag agggatggtt agctcggttt cctatgtttg actgggttgg  120

tggtaggact tcagaaatgt cagctgttgg tttacttcca gctgcattgc agggtattga  180
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212

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<400>        628

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tttgattggg ttggtggtag gacttcagaa atgtcagctg tgggtttact tccagctgca   180

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tgctgaggca cttgcgcctg ataaccctcc actgaagata agatttattg acaacaccga   180

tcctgctggg attgatcatc aaattgctca actaggacct gaactggcaa ctactcttgt   240

aattgtcatt tctaagagcg gaggcacacc tgaaacccgc aatgggctac tggaag       296


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taagatttat tgacaacaca gatcctgctg ggattgatca tcaaattgct caactaggac   180

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213

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agattctttc cccatctggt cgtttcactt caattctctc tataggaatc ggagggtcag   120

ctttgggccc tcaatttgtt gctgaggcac ttgcgcctga taaccctcca ctgaagataa   180

gatttattga caacaccgat cctgctggga ttgatcatca aattgctcaa ctaggacctg   240

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atcaatgcct atcatcagcc tggtgttgag gctgggaaaa aggcagcagg agaagtattg   180

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ccattgactc tagatgaaat tgcagatcgc tgc   273

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tatagatgaa attgcagatc gctgccattg ccctgaagat attgagatga tctacaaaat   180

agtccagcac atggctgcta cgacagagc aatcatagca gaaggcagct gtggctctcc   240

214

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ggttccgagc ctggatccgt gt   322

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<212>   DNA
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atgaaattgc agatcgctgc cattgccctg aagatattga gatgatctac aaaatagtcc   180

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gcgttaaggt gtacctcggt gaat   264

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ttcgacctgg atggcaaccg tgttaatcaa gggctaactg tatatggtaa caaaggaagc   120

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gaccgggagt   310

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215

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ttggagcact ggttgcactt tatgaacgtg ctgtggggct ttatgcttct ttg           293


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actcctagag ctgttggagc actgattgca ctttatgaac gtgctgtggg gatttatgct   240

tctttggtaa atatcaatgc ctatcatcag cctggtgttg a                       281


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atcagaaggg ataggcaata aggatatggt tgtacttcct tacaaggata gtttgttgct   120
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216

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cgcttacatt cagcagctga gag                                           263


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caataaggat atggttgtac ttccttacaa ggatagtttg ttgcttttga gtagatattt   180

gcaacaactt gtcatggaat ctcttgggaa agaatttgat ctggatggca accgggtaaa   240

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caaggatagt ttgttgcttt tgagtagata tttgcaacaa cttgtcatgg aatctcttgg   240

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217

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tgcttcctta taaggatagt ttgttacttt tgagtagata tttgcaacaa cttgtcatgg   180

gatctcttgg aaaagaattc gacctggatg gcaaccgtgt taaacaaggg ctaactgtat   240

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gagtctatct ctgttacgtg caagaggtaa ctcctagagc tgttggagca ctgatttcac   180

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<212>   DNA
<213>   Zea mays

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218

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caataaggat atggttgtac ttccttacaa ggatagtttg ttgcttttga gtagatattt   180

gcaacaactt gtcatggaat ctcttgggaa agaatttgat ctggatggca accgggtaaa   240

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gctgag   306

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gcagggaaca cgttctgctc tttatgcaaa tgaccgtgaa tctatctctg ttactgtgca   180

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atgttgcagg gaacccgttc tgctctttat gcaaatgacc gggagtctat ctctgttact   180

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<400>   650

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cccggaacac tgtggttaaa gaaaatccag cagcattgct tgcattatgt tggtattggg   120

catcagaagg gataggcaat aaggatatgg ntgtacttcc ttacaaggat agtttgttgc   180

ttttgagtag atatttgcaa caacttgtca tggaatctct tgggaagaat tgatctggat   240

gcaaccggta aatcaaggct atctgatatg aaacaaagaa gactg   285

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<212>   DNA
<213>   Zea mays

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ttcttcattt tgggagttat cacagagcca gtttggcagt gctgtagttt tggttttacc   180

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agcacgcagc atgatgaaac atattta   267

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gagcagtgga aggccctcca ggcgcacgtc ggcgcgattc agaagacgca cctgcgcgac   180

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<213>   Zea mays

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221

cggaagccat ggcgtcggca cgctaatct cggcacgga gcagtggaag gccctccagg   180

cgcacgtcgg cgcgattcag aagacgcacc tgcgcgacct gatggccgac gccgaccgat   240

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tgtctccccc gaccggcgat cgctatcgac ttgtagcgga agccatggcg tcggcagcgc   180

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acgagggtcg catggtgggc cactactggc tccgcgaccc ggccctcgct cccaactcct   240

222

tcctccggaa caagatcgag accgcac   267

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gtaacgggaa gggtgtttcc attgatggcg cccaactttc ctttgagaca ggtgaaattg 120

attttggtga acctcgaact aatggccagc acagcttcta tcaattaatc catcagggaa 180

gggttatccc ttgcgacttt attggtgttg ttaaaagtca gcagcctgtt tacttgaaag 240

gggaaactgt gagtaatcat gatgagctta tgtccaattt ctttgcccaa cctgatgctc 300

ttgcttatgg aaagactcct gaaca   325

tccagctagg gcaatattgc catattctca ggcacttgag aagttggcac cacatataca   60

gcagcttagc atggagagta acgggaaggg tgtttccatt gatggcgccc aactttcctt 120

tgagacaagt gaaattgatt ttggtgaacc tggaactaat ggccagcaca gcttctatca 180

attaatccat caggaaggg ttatcccttg cgactttatt ggtgttgtta aaagtcagca 240

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tgcccaacct gatgct   316

atcaaagaca ttcacaacag ctgnaaacaa tgttaaatgc tcgaactctt aaggagtgga   60

tcgtttcttc tcttgggcca caggctgttg ccaaacatat gattgctgtc agcactaatc 120

ttaagcttgt gaaggagttt ggaattgacc caaacaatgc ttttgccttt tgggactggg   180

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<212>   DNA
<213>   Zea mays

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agggcaaccg gccatcacta agtttgcttc tgcctacact atctgcatat gaggttggac   180

agcttttatc catctatgag caccggattg cagttcaggg cttcatatgg ggaattaact   240

catttgacca ctagggagtg gagctaggga agtcactcgc ttctcaagtg aggaaacagc   300

tgcatggaac ccggatggaa ggacacctgt tgag   334

<210>   662
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<212>   DNA
<213>   Zea mays

<400>   662

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atcccttgcg actttattgg tgttgttaaa agtcagcagc ctgtttactt gaaagggga   120

actgtgagta atcatgatga gcttatgtcc aatttctttg cccaacctga tgctcttgct   180

tatggaaaga ctcctgaaca gttgcacagt gagaaagttc cagaaaatct tatccctcat   240

aagactttta agggcaaccg gccatcacta agtttgctt   279

<210>   663
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<212>   DNA
<213>   Zea mays

<400>   663

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224

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tcttaaggag tggatcgttt cttctcttgg gccacaggct gttgccaaac atatgattgc   180

tgtcagcact aatcttaagc ttgtgaagga gtttggaatt gacccaaaca atgcttttgc   240

cttttgggac tgggttggcg gccgttatag tgtt                              274


<210>      664
<211>      283
<212>      DNA
<213>      Zea mays

<223>      unsure at all n locations
<400>      664

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gtttggaatt ganccaaaca atgcttntgc ctnttgggac tgggttggcg gccgttatag   120

tgtttgcagt gctgttggcg ttctgccatt atctcttcag tatggcttgc caattgtcca   180

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<213>      Zea mays

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gtttggaatt gacccaaaca atgcttttgc cttttgggac tgggttggcg gccgttatag   120

tgtttgcagt gctgttggcg ttctgccatt atctcttcag tatggctttc caattgtcca   180

gaaatttttg gagggagctt ccagcattga caaccacttc tactcatctt catttgagaa   240

aaatataccg tacttcttgg tttgctgag                                   269


<210>      666
<211>      299
<212>      DNA
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225

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ataggtggta gctttcttgg ccctctattt gtgcatactg cactccagac cgatccagaa   120

gcagcagaat gtgcaaaagg ccggcaactg agattccttg caaatgttga tccagttgac   180

gttgcacgaa gcattaaaga tttggatcca gaaaccactc tggtggtggt tgtatcaaag   240

acattcacaa cagctgaaac aatgttaaat gctcgaactc ttaaggagtg gatcgtttc   299

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<212>   DNA
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<400>   667

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tttgcagtgc tgttggcgtt ctgccattat ctcttcagta tggctttcca attgtccaga   120

aatttttgga gggagcttcc agcattgaca accacttcta ctcatcttca tttgagaaaa   180

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tagggcaata tgccatatct caggcacttg agaagt   276

<210>   668
<211>   255
<212>   DNA
<213>   Zea mays

<400>   668

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ctggaaaacc gttgacaaat gttgtgtcgg ttggaatagg tggtagcttt cttggccctc   180

tatttgtgca tactgcactc cagaccgatc cagaagcagc agaatgtgca aaaggccggc   240

aactgagatt ccttg   255

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<212>   DNA
<213>   Zea mays

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acttcttggt ttgctgagtg tgtggaatgt ttcatttctt ggttatccag ctagggcaat   180

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<210>      670
<211>      191
<212>      DNA
<213>      Zea mays

<223>      unsure at all n locations
<400>      670

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gagaaagttc cagaaaatct tatccctcat aagactttta agggcaaccg gccatcacta   120

agtttgcttc tgcctacact atccgcatat gaggtggaca gttttaancc tctatngggc   180

ncggtttnan t                                                        191


<210>      671
<211>      115
<212>      DNA
<213>      Zea mays

<400>      671

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cagaatgtgc aaaaggccgg caactgagat tccttgcaaa tgttgatcca gttga         115


<210>      672
<211>      113
<212>      DNA
<213>      Zea mays

<223>      unsure at all n locations
<400>      672

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tagtgtttgc agtgctgttg gcgntctgcc attatctctt cagtatggct ttc          113


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<212>      DNA
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227

<210> 673

<213>   Zea mays

<400>   673

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tc   122

<210>   674
<211>   443
<212>   DNA
<213>   Zea mays

<223>   unsure at all n locations
<400>   674

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tttatgaacg tgctgtgggg atttatgctt ctttggtaaa tatcaatgcc tatcatcagc   120

ctggtgttga ggctgggaaa aaggcancan gagaagtatt ggcccttcag aaaagggttc   180

tgactgtatt aaaggaggcc atctgcnaga accctactga gccattgact ctagatgaaa   240

ttgcagatcg ctgacattgc cctgaagata ttganatgat ctacanaata atccancaca   300

tggcttctaa cgacagatca cttatagcag aaggcatctg cngctttctt ngcagtgtta   360

aggtgtacct nggtgaaatg caattttgga ccnaantatg caggccggga tagattctgn   420

gtcnggancn aagtaacatt ntt   443

<210>   675
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<212>   DNA
<213>   Zea mays

<400>   675

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gaaacaaagg aagcactgac cagcacgctt acattcagca gctgagagaa ggtgtacaca   120

acttctttgt tacttttatc gaggtcttgc gtgacaggcc tgctggtcat gattgggagc   180

ttgaacctgg agtcacatgt ggtgactatt tgtttgggat gttgcaggga acacgttctg   240

ctctttatgc aaatgaccgt gaatctatct ctgttactgt gcaagaggta actcctagag   300

ctgttggagc actggttgca ctttatgaac gtgctgtggg gctttatgct tctttggtaa   360

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<210>      676
<211>      349
<212>      DNA
<213>      Zea mays

<400>      676

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ttgtttttga catgccaatt gctgagttct gacttggcaa ggttgagcat aagtctttct  120

tcatttggga gttatcacag agccagtttg gcagtgctgt agttttggtt ttacctactc  180

tttgtagaag aaaagtgaag agtggatatt atggaacaaa atatatacct acggcagcac  240

gcagcatgat gaaacatatt taaaaaattt gggtgctcta ccacatgccc gtggaataaa  300

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<210>      677
<211>      376
<212>      DNA
<213>      Zea mays

<223>      unsure at all n locations
<400>      677

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aagcagatcc gtctcccccg agccccgacc ggcgatcgct atcgacttgt agcggaagcc  120

atggcgtcgg cagcgctaat ctgcggcacg gagcagtgga aggccctcca ggcgcacgtc  180

ggcgcgattc agaagacgca cctgcgcgac ctgatggccg acgccgaccg atgcaaggca  240

atgacggctg agtatgaagg gatctttctg gattactcga gacagcaggc gactggtgaa  300

accctggaga agctccttaa atgggctgac gctgcgaagc tcaaggagaa ngatgagaag  360

atgtttaaag gtgaaa                                                  376


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<212>      DNA
<213>      Zea mays

<400>      678
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229

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ttggttatcc agctagggca atattgccat attctcaggc acttgagaag ttggcaccac   240

atatacagca gcttagcatg gagagtaacg gaagggtgt ttccattgat ggcgcccaac    300

tttcctttga dacaggtgaa attgattttg gtgaacctgg aactaatggc cagcacagct   360

tctatcaatt aatccatcaa ggaagggtta tcccttgcga ctttattggt gttgttaaaa   420

gtcagcagcc tgtttacttg aaaagggaaa c                                   451


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cttgcgactt tattggtgtt gttaaaagtc agcagcctgt ttacttgaaa ggggaaactg   240

tgagtaatca tgatgagctt atgtccaatt tctttgccca acctgatgca cttgcttatg   300

gaaagactcc tgaacagttg cacagtgaga aagttccaga aaatcttatc cctcataaga   360

cttttaaggg caaccggcca tcactaagtt tgcttctgcc tacactatcc gcatatgagg   420

ttggacagct tttatccatc tatgagcacc gga                                 453


<210>        680
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<212>        DNA
<213>        Zea mays

<400>        680

aaaatcaagc agttttcaga gactttttaga agtggatcat gggttggagc aactggaaaa    60

ccgttgacaa atgttgtgtc agttggaata ggtggtagct ttcttggccc tctatttgtg   120

catactgcac tccagaccga tccagaagca gcagaatgtg caaaaggccg gcaactgaga   180
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230

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ttccttgcaa atgttgatcc agttgacgtt gcacgaagca ttaaagattt ggatccagaa    240

accactctgg tggtggttgt atcaaagaca ttcacaacag ctgaaacaat gttaaatgct    300

cgaactctta aggagtggat cgtttcttct cttgggccac aggctgttgc caaacatatg    360

attgctgtca gcactaatct taagcttgtg aaggagtttg gaattgaccc aaacaatgc     419


<210>        681
<211>        426
<212>        DNA
<213>        Zea mays

<400>        681

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ggaagggtgt ttccattgat ggcgcccaac tttcctttga cacaggtgaa attgattttg    180

gtgaacctgg aactaatggc cagcacagct tctatcaatt aatccatcag ggaagggtta    240

tcccttgcga ctttattggt gttgttaaaa gtcagcagcc tgtttacttg aaaggggaaa    300

ctgtgagtaa tcatgatgag cttatgtcca atttctttgc ccaacctgat gctcttgctt    360

atggaaagac tcctgaacag ttgcacagtg agaaagttcc agaaaatctt atccctcata    420

agactt                                                               426


<210>        682
<211>        323
<212>        DNA
<213>        Zea mays

<400>        682

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aacaggtcag tgcttcatgt agctctgagg gctccaagag atgcagtcat aaacagtgat    120

ggggtgaatg tggtccctga ggttcggagt gttaaagata aaatcaagca gttttcagag    180

acttttagaa gtggatcatg ggttggagca actggaaaac cgttgacaaa tgttgtgtcg    240

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<210>        683
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231

<211>   422
<212>   DNA
<213>   Zea mays

<223>   unsure at all n locations
<400>   683

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ttggntccag aaaccacccn ggtggtggtt gtancaaaga cattcacaac agcggaaaca   120

atgttaaatg ctcgaactct taaggagtgg atcgtttctt ctcttgggcc acaggctgtt   180

gccaaacata tgattgctgt cagcactaat cttaagcttg tgaaggagtt tggaattgac   240

ccaaacaatg cttttgcctt ttgggactgg gttggcggcc gttatagtgt ttgcagtgct   300

gttggcgttc tgccattact cttcagtatg gctttccaat tgtccagaaa tttttggagg   360

gaacttccag ncattgacaa acaacttcna ntcnncctnc attttgagaa aaatatacct   420

gt   422

<210>   684
<211>   122
<212>   DNA
<213>   Glycine max

<223>   unsure at all n locations
<400>   684

ggtgagtaac catgatgagc taatgtccaa ctattttgca cagtctgatg cccttgcata   60

tnnnaagaca gcagagcagc tgcnaaaggn caatgtttcc ccgcacctta ttccacacaa   120

ga   122

<210>   685
<211>   234
<212>   DNA
<213>   Glycine max

<400>   685

tgataatcct ccactcaaga taacatacat ggacaacacg gatcctgctg gaattgatca   60

tcagattgca caacttgggc ctgagctagc ttcaacactt gtgattgtga tatcaaagag   120

tggaggtact cctgagacca gaaatggttt attggaagtg cagaaggcct tcgtgaagc   180

aggcttggat tttcctaaac agggtgttgc tataacacaa gaaaattctt tgtt   234

232

<210> 686
<211> 205
<212> DNA
<213> Glycine max

<223> unsure at all n locations
<400> 686

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cagcagccct tccagggatt ganatnanag aaatgcttgc cggtgcatca ttgatggatg   120

angctaanag gagtactgtg nnaaggaata accctgcagc tctgctggct ttatgttggt   180

attgggctac agatggtgna ggatc                                        205
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<210> 687
<211> 223
<212> DNA
<213> Glycine max

<400> 687

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tgcagggcgt tgctataact caagaaaatt ctttgctgga taacactgca agaattgagg    60

gttggttagc tagatttcca atgtttgact gggtgggagg tagaacatca gagatgtctg   120

cagtgggcct gcttccagca gcccttcaga gcattgacat aagagaaatg cttgctggtg   180

cagcattaat ggatgaggcg aataggagta ctgtgataag gaa                    223
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<210> 688
<211> 218
<212> DNA
<213> Glycine max

<400> 688

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gttggttagc tagatttcca atgtttgact gggtgggagg tagaacatca gagatgtctg   120

cagtgggcct gcttccagca gcccttcaga gcattgacat aagagaaatg cttgctggtg   180

cagcattaat ggatgaggcg aataggagta ctgtgata                          218
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<210> 689
<211> 274
<212> DNA
<213> Glycine max

233

<400>   689

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tgactacttg tttggtatgc tacagggaac aagatcagct ctgtatgcca ataaccgaga   120

gtccatcaca gttactgtac aagaagtgac acctagaaca gttggtgctc ttattgcact   180

ctatgaacga gcagtaggaa tttatgcctc ccttgtcaac ataaatgctt atcatcaacc   240

aggtgtggaa gctggtaaaa aagcagcagg tgaa   274

<210>   690
<211>   257
<212>   DNA
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<400>   690

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gacctcctgg tcatgattgc gaacttgaac ctggtgtcac atgcggtgac tacttgtttg   120

gtatgctaca gggaacaaga tcagctctgt atgccaataa ccgagagtcc atcacagtta   180

ctgtacaaga agtgacacct agaactgttg gtgctcttat tgcactctat gaacgagcag   240

taggaattta tgcctcc   257

<210>   691
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<212>   DNA
<213>   Glycine max

<223>   unsure at all n locations
<400>   691

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acaaggtcgg ctttgtatgc caataaccga gagtccatca cagttactgt acaagaaggg   120

acaccaagaa cagttggtgc tcttattggg ctctatgaac gagcagtagg aatttatgcc   180

tcccctgtca acataaatgc ttatctnaac ctgcgtgtgg aagntgacga natnagcagc   240

agngaagtac t   251

<210>   692
<211>   245
<212>   DNA

234

<213>   Glycine max

<223>   unsure at all n locations
<400>   692

atcctgcanc tttgcnggct ttatgttggt attgggctac agatggtgta ngatcaaaag   60

atatggttat ccttccatat aaggacagct nganattatn tagtagatac ttgcaacagt   120

nggtcatgga atctctaggc aaggagtttg actgaatggt aatcgggtta atcaaggaat   180

tagtgtctat ggaaataaag gaagcacaga tcagcatgcc tacatccaac aactgaggga   240

aggtg   245

<210>   693
<211>   270
<212>   DNA
<213>   Glycine max

<400>   693

cagcatgcct acattcagca actgagggaa ggtgtgcaca attttttttgt gacattcatt   60

gaggtgctac gcgatagacc acctggtcat gattgggagc ttgaaccagg tgtcacatgt   120

ggtgactacc tgtttggtat gctacaggga acaaggtcag ccctgtatgc caataaccgt   180

gaatccatca ctgtcacagt gcaagaagtg acacccagat cagttggtgc ccttgtagcc   240

ctttatgaac gggccgttgg aatatatgct   270

<210>   694
<211>   259
<212>   DNA
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<400>   694

ggagtttgac ttgaatggta atcgggttaa tcaaggaatt agtgtctatg gaaataaagg   60

aagcacagat cagcatgcct acattcaaca actgagggaa ggtgtgcaca attttttttgt   120

gacattcatt gaggtgctac gcgatagacc acctggtcat gattgggagc ttgaaccagg   180

tgtcacatgt ggtgactacc tgtttggtat gctacaggga acaaggtcag ccctgtatgc   240

caataaccgt gaatccatc   259

<210>   695
<211>   227

<212> DNA
<213> Glycine max

<400> 695

atagaagtac tgtgttaagg aataaccctg cagctctgct ggctttatgt tggtattggg   60

ctacagatgg tgtaggatcc aaggatatgg ttattcttcc gtacaaggac agcctgttat   120

tattcagtag atacttgcag cagctggtca tggaatctct aggcaaggag tttgacttgg   180

atggtaatcg ggttaatcaa ggaattagtg tctatggaaa caaagga   227

<210> 696
<211> 263
<212> DNA
<213> Glycine max

<223> unsure at all n locations
<400> 696

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gaagtactgt gttaaggaat aaccctgcag ctntgctggc ttangnaagg tattgggcta   120

cagatggtgt aggaccaagg anatggttat cttccgtac aaggacagcc tngtattatt   180

cagtagatac ntgcagcagc tggtcatgga atctctaggc aaggagtttg acttggatgg   240

taatcgggtt aatcaaggaa tag   263

<210> 697
<211> 266
<212> DNA
<213> Glycine max

<400> 697

gcgcgatcgc gaatcccgat gagagtcgca tggtgggaca ctattggctg agggaccncta   60

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agttcgctaa cgacgtcgtt agtggtaaga ttaagcctcc ttcgtctccg gagggtcgat   180

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aagcattggc acctgataat cctcca   266

<210> 698
<211> 398
<212> DNA

236

<213>   Glycine max

<223>   unsure at all n locations
<400>   698

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gctttatgtt ggtattgggc tacagatggt gtaggatcaa aagatatggt tatccttcca   120

tataaggaca gcttgttatt atttagtaga tacttgcaac agttggtcat ggaatctcta   180

agcaaggagt ttgacttgaa tggtaatcgg gttaatcaag gaattagtgt ctatggaaat   240

aaaggaagca cagatcagca tgcctacatt cagcaactga nggaaggtgt gcacaatttt   300

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caagtgtcac atgtggtgac tacctgtttg gtatgcta   398

<210>   699
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<400>   699

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gagggaccct aagcgtgcgc ccaactcgtt ccttaaaacg cagattgaga cactctcga   120

cgctgtttgc aagttcgcta acgacgtcgt tagtggtaag attaagcctc cttcgtctcc   180

ggagggtcga tttactcaaa tattgtctgt gggaattgga agttctgctc ttggaccaca   240

gtttgttgca gaagcattgg cacctgataa tcctccactc aagataagat ttgtggacaa   300

cacggatcct gctggaattg atcatcagat tgcacaactt gggcctgagc tagcttcaac   360

ac   362